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FILE 'MEDLINE' ENTERED AT 17:02:18 ON 29 SEP 2004

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=> s database and (cell or plant or culture)
L1 20383 DATABASE AND (CELL OR PLANT OR CULTURE)

=> s l1 and time course
L2 58 L1 AND TIME COURSE

=> s l2 and py<2000
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L4 ANSWER 1 OF 11 MEDLINE on STN DUPLICATE 1
AN 1999134133 MEDLINE
DN PubMed ID: 9950599
TI Oxidative stress induces differential gene expression in a human lens epithelial **cell** line.
AU Carper D A; Sun J K; Iwata T; Zigler J S Jr; Ibaraki N; Lin L R; Reddy V
CS Laboratory of Mechanisms of Ocular Diseases, National Eye Institute, National Institutes of Health, Bethesda, Maryland 20892, USA.
SO Investigative ophthalmology & visual science, **(1999 Feb)** 40 (2) 400-6.
Journal code: 7703701. ISSN: 0146-0404.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199902
ED Entered STN: 19990223
Last Updated on STN: 19990223
Entered Medline: 19990210
AB PURPOSE: To identify differentially expressed genes in a human lens epithelial **cell** line exposed to oxidative stress. METHODS: Reverse transcriptase-polymerase chain reaction (RT-PCR) differential display was used to evaluate differential gene expression in a human lens epithelial **cell** line (SRA 01-04) when **cells** were exposed for 3 hours to a single bolus of 200 microM hydrogen peroxide. Differentially expressed genes were identified through DNA sequencing and a nucleotide **database** search. Differential expression was confirmed by northern blot and RT-PCR analyses. RESULTS: Using 18 primer sets, 28 RT-PCR products were differentially expressed between control and hydrogen peroxide-treated **cells**. In stressed **cells**, mitochondrial transcripts nicotinamide adenine dinucleotide (NADH) dehydrogenase subunit 4 and cytochrome b were downregulated 4-fold. Of the cytoplasmic mRNAs, glutamine cyclotransferase decreased 10-fold, whereas cytokine-inducible nuclear protein, alternative splicing factor 2, and beta-hydroxyisobutyryl-coenzyme A hydrolase increased 2-, 4-, and

10-fold, respectively. Analysis of mitochondrial transcripts in a 24-hour time course showed that NADH dehydrogenase subunit 4 mRNA decreased by 2-fold as early as 1 hour after oxidative stress, whereas the rate of decrease was slower for cytochrome b, cytochrome oxidase III, and 16S rRNA. CONCLUSIONS: Oxidative stress induced specific expressed gene changes in hydrogen peroxide-treated lens cells, including genes involved in cellular respiration and mRNA and peptide processing. These early changes may reflect pathways involved in the defense, pathology, or both of the lens epithelium, which is exposed to oxidative stress throughout life.

L4 ANSWER 2 OF 11 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1998:509495 BIOSIS
DN PREV199800509495
TI On-line recognition and control of physiological state by computing intelligence in fermentation processes-monograph.
AU Shimizu, Hiroshi [Reprint author]
CS Dep. Biotechnol., Graduate Sch. Eng., Osaka Univ., 2-1 Yamadaoka, Suita, Osaka 565-0871, Japan
SO Seibutsu-Kogaku Kaishi, (1998) Vol. 76, No. 8, pp. 338-348. print. ISSN: 0919-3758.
DT Article
LA Japanese
ED Entered STN: 18 Dec 1998
Last Updated on STN: 18 Dec 1998
AB The application of computing intelligence, specifically fuzzy logic and a neural network, to feature capturing, state recognition, fault diagnosis, and control in bioprocesses is discussed through three examples of Saccharomyces cerevisiae fermentations. The ethanol concentration in a fed-batch culture was controlled by a newly developed fuzzy controller that is also to diagnose the status of the glucose concentration in the medium, i.e., the depletion or overfeeding of glucose, using not only the ethanol concentration data but also the carbon dioxide concentration in the exhaust gas. As a result, the control performance was much improved and overaction of the controller was avoided. A fuzzy physiological state recognition system was developed as a powerful tool to capture the physiological states in the fed-batch fermentation process. The error vector was newly defined in the macroscopic elemental balance. The physiological states were characterized by a database of error vectors, and membership functions for state recognition were constructed based on the error vectors. The physiological states could be recognized, including an abnormal case in which aerobic ethanol production occurred with low growth. A technique for the integration of fuzzy logic and mathematical and stoichiometric analysis is also discussed. A novel neural network-an autoassociative neural network (AANN)-was applied to fault diagnosis in an alpha-amylase production process using a temperature-sensitive mutant of Saccharomyces cerevisiae. Faults and uncertainties, such as faulty sensors and plasmid instability, significantly affected the performance of the optimized process. The autoassociative neural network was trained so that the network inputs were reproduced at the output layer. The features of the time courses of the state variables in "good" fermentations were captured by the AANN, and the data from "bad" fermentations could be discriminated successfully. By implementing corrective action after fault detection, performance was recovered and the final production amount was increased.

L4 ANSWER 3 OF 11 MEDLINE on STN DUPLICATE 2
AN 1998036063 MEDLINE
DN PubMed ID: 9370296

TI Upregulation of a novel gene by freezing exposure in the freeze-tolerant wood frog (Rana sylvatica).
AU Cai Q; Storey K B
CS Institute of Biochemistry and Department of Biology, Carleton University, Ottawa, Ontario, Canada.
NC GM 43796 (NIGMS)
SO Gene, (1997 Oct 1) 198 (1-2) 305-12.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U44831
EM 199712
ED Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971209
AB A novel gene responsive to freezing exposure was identified among five cDNA clones obtained through differential screening of a cDNA library constructed from liver of frozen wood frogs. The cDNA sequence of this gene, cloned in the recombinant plasmid, pBfFR14, showed no homology to any genes available in the Genbank database. The clone, designated as Fr10, carried a 457 bp cDNA sequence and contained a single open reading frame that could potentially encode a small protein of 90 amino acids with a molecular weight of about 10 kDa, named FR10. The putative protein contained a highly hydrophobic N-terminal region (21 residues) that carries a potential nuclear exporting signal (NES) sequence, LALVVLVIAISGL, similar to the NES found in PKI, an inhibitor of protein kinase A (PKA). A single mRNA transcript with a size of 550 nt was detected when the insert of the pBfFR14 was used as a probe against the Northern blot containing total RNA isolated from wood frog organs. RNA blotting analysis for gene expression in eight organs showed that transcription of the gene was highly induced by 24 h of freezing exposure at -2.5 degrees C in liver and gut, moderately elevated in heart, lung, brain and bladder but showed no change in skeletal muscle and decreased in kidney. A time-course analysis for freezing regulation of gene expression in liver showed that transcript levels were increased by 2-fold in 1 h of freezing exposure and the levels continued to increase up to 3.5-fold over the control after 24 h of freezing exposure, but had returned to control levels after 24 h thawing at 5 degrees C. Gene expression in liver was also up-regulated by whole animal dehydration at 5 degrees C but strongly down-regulated by anoxia exposure, indicating that the gene may respond to cell volume regulatory signals in vivo during natural freezing.

L4 ANSWER 4 OF 11 MEDLINE on STN DUPLICATE 3
AN 97073251 MEDLINE
DN PubMed ID: 8915999
TI The cDNA sequence of porcine vitronectin and its expression in liver and skeletal muscle of GH-supplemented pigs.
AU Hanazono M; Ozawa A; Yasue H
CS Department of Clinical Research of Ichihara Hospital, School of Medicine, Teikyo University, Chiba, Japan.
SO Journal of veterinary medical science / the Japanese Society of Veterinary Science, (1996 Oct) 58 (10) 989-94.
Journal code: 9105360. ISSN: 0916-7250.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-D61396

EM 199707
ED Entered STN: 19970721
Last Updated on STN: 19970721
Entered Medline: 19970708
AB A cDNA (1555 bp) (DNA **database** accession number, D61396) having a homology with human vitronectin (Vn) was isolated from a porcine liver cDNA library, and its sequence was determined. The open reading frame in the cDNA was found to code a protein with 388 amino acids, then the amino acid sequence of the protein (porcine putative Vn) was aligned to the other mammalian (mouse, rabbit, and human) Vns previously reported. The alignment revealed that the functional amino acid sequences reported as the **cell** attachment site, the heparin binding site, the region involved in glycosylation, and plasminogen activator inhibitor I-binding domain were conserved in the porcine putative Vn. These findings together with the fact that the calculated molecular weight and the N-terminal amino acid sequence of the putative Vn agreed with those reported by biochemical analysis on porcine Vn, led us to conclude that the cDNA isolated in the present study coded for the porcine Vn. Then, a **time course** study was performed to examine whether the administration of growth hormone (GH) affects Vn mRNA expression in liver and skeletal muscle, since the level of Vn mRNA was reported to be affected by inflammation, and since GH was reported to be involved in inflammation. This revealed that GH has no effect on the level of liver Vn mRNA, and that Vn mRNA level in skeletal muscle seemed to be affected following GH-injection.

L4 ANSWER 5 OF 11 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:410254 BIOSIS
DN PREV199699132610
TI A model of the gas exchange response of Picea abies to habitat conditions.
AU Falge, E.; Graber, W.; Siegwolf, R.; Tenhunen, J. D. [Reprint author]
CS Bayreuth Inst. Terrestrial Ecosystem Res., Univ. Bayreuth, D-95440 Bayreuth, Germany
SO Trees (Berlin), (1996) Vol. 10, No. 5, pp. 277-287.
CODEN: TRESEY. ISSN: 0931-1890.
DT Article
LA English
ED Entered STN: 10 Sep 1996
Last Updated on STN: 10 Sep 1996
AB **Databases** describing branch gas exchange of Picea abies L. at two montane forest sites, Lageren, Switzerland (National Forschungsprojekt 14 of the Schweizerische Nationalfonds) and Oberwarmensteinach, Germany (Bayerische Forschungsgruppe Forsttoxikologie), were analyzed in conjunction with a physiologically based model. Parameter estimates for describing carboxylase kinetics, electron transport, and stomatal function were derived, utilizing information from both single factor dependencies and diurnal **time course** measurements of gas exchange.
Data subsets were used for testing the model at the branch level. Most of the observed variation in gas exchange characteristics can be explained with the model, while a number of systematic errors remain unexplained. Factors seen as contributing to the unexplained residual variation and not included in the model are light acclimation, degree of damage in adjustment to pollutant deposition, needle age, and cold stress effects. Nevertheless, a set of parameter values has been obtained for general application with spruce, e. g., for use in calculating canopy flux rates and to aid in planning of focused leaf and canopy level experiments. The value of the model for estimating fluxes between the forest and the atmosphere must be evaluated together with measurements at the stand level.

L4 ANSWER 6 OF 11 MEDLINE on STN DUPLICATE 4
AN 95029892 MEDLINE
DN PubMed ID: 7943332
TI Secretagogue regulation of pancreatic acinar cell protein phosphorylation shown by large-scale 2D-PAGE.
AU Wishart M J; Groblewski G; Goke B J; Wagner A C; Williams J A
CS Department of Physiology, University of Michigan Medical School, Ann Arbor 48109-0622.
NC 5T32-GM08322 (NIGMS)
DK-41122 (NIDDK)
P30-DK-34933 (NIDDK)
+
SO American journal of physiology, (1994 Oct) 267 (4 Pt 1) G676-86.
Journal code: 0370511. ISSN: 0002-9513.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199411
ED Entered STN: 19941222
Last Updated on STN: 19970203
Entered Medline: 19941122
AB High-resolution large-scale two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) combined with computer-assisted image analysis was used to construct a database of secretagogue/second messenger-induced phosphoprotein modifications in intact rat pancreatic acinar cells. Isolated acini were labeled with 32Pi, exposed to hormones and other test agents, and subjected to large-scale 2D-PAGE and autoradiography. This procedure resolved 500 phosphoproteins in pancreatic acinar whole cell lysates, approximately 90% of which were localized in the soluble fraction of centrifuged samples. Soluble proteins were further characterized as to heat and acid stability. Cholecystokinin (CCK), carbachol, and bombesin altered the phosphorylation state of about 27 proteins with both increases and decreases observed. Subsets of proteins were phosphorylated in response to phorbol ester 12-O-tetradecanoylphorbol 13-acetate (TPA), calcium ionophore A-23187, and adenosine 3',5'-cyclic monophosphate (cAMP) analogue 8-bromo-cAMP. One of these proteins was identified as the myristoylated, alanine-rich, C-kinase substrate (MARCKS) protein by immunoprecipitation. The time course and dose response of phosphorylation changes due to CCK showed considerable variation between proteins, although a temporal hierarchy of phosphorylation events was clearly exhibited. Particularly striking was the rapid dephosphorylation within 30 s of a 19-kDa soluble protein to a minimum of 20 +/- 1% of control. Increased phosphorylation of the MARCKS and other TPA-regulated proteins suggests that CCK, carbachol, bombesin, and the CCK partial agonist, JMV-180, all activate protein kinase C in intact acini.

L4 ANSWER 7 OF 11 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1995:77040 BIOSIS
DN PREV199598091340
TI An on-line advisory control system for the lactic acid fermentation process.
AU Nakajima, M. [Reprint author]; Von Numers, C.; Yada, H.; Siimes, T.; Pokkinen, M.; Endo, I.; Linko, P.
CS Chem. Eng. Lab., RIKEN, Wako-shi 2-1, Saitama 351-01, Japan
SO Applied Microbiology and Biotechnology, (1994) Vol. 42, No. 2-3, pp. 204-211.
CODEN: AMBIDG. ISSN: 0175-7598.
DT Article

LA English
ED Entered STN: 22 Feb 1995
Last Updated on STN: 23 Feb 1995
AB A fuzzy expert system was developed for on-line diagnosing and controlling of bioprocesses. The system was constructed in object-oriented Smalltalk/V for diagnosing and controlling of bioprocesses. Lactic acid fermentation with an industrial strain of Lactobacillus casei was chosen as the model system. The performance of the fuzzy expert system and the knowledge base utilizing experts' knowledge and several facts obtained from the experiments were successfully validated with on-line fermentations. The fuzzy expert system could diagnose a fault on-line and give reasonable advice to the process operator. In order to achieve the diagnosing faculty, a database, a knowledge base, and both backward and forward chaining procedures were implemented employing the object-oriented programming environment. A defuzzifier was implemented in the system to achieve on-line control. In order to realize a decision-making system with a human operator and a fuzzy expert system, a new control strategy named Advice was also introduced. Several cultivations were carried out in order to collect knowledge on the effects concerned with inoculum properties to the process and to construct a database including standard time-course profiles. The performance of the fuzzy expert control system was successfully tested with on-line experiments.

L4 ANSWER 8 OF 11 MEDLINE on STN DUPLICATE 5
AN 94368869 MEDLINE
DN PubMed ID: 8086474
TI Isolation and characterization of a novel cDNA from HL-60 cells treated with 1,25-dihydroxyvitamin D-3.
AU Chen K S; DeLuca H F
CS Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.
NC DK-14881 (NIDDK)
SO Biochimica et biophysica acta, (1994 Sep 13) 1219 (1) 26-32.
Journal code: 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-S73591
EM 199410
ED Entered STN: 19941031
Last Updated on STN: 19970203
Entered Medline: 19941020
AB A novel cDNA clone (VDUP1) has been isolated from a cDNA library constructed from mRNA obtained from HL-60 cells stimulated by 1,25-dihydroxyvitamin D-3. Northern blot analysis showed that VDUP1 cDNA hybridizes to a 2.9 kb mRNA species which is up-regulated in HL-60 cells by 1,25-dihydroxyvitamin D-3 (1,25-(OH)2D3) treatment. In vitro expression of VDUP1 cDNA produced a 46 kDa protein. A search of the GenBank database revealed that the 3' untranslated region of VDUP1 is homologous to a sequence expressed in brain. A detailed time course study showed that the VDUP1 mRNA starts to increase at 6 h after 1,25-dihydroxyvitamin D-3 treatment, reaches a plateau at around 18 h and stays elevated for 24 h. The VDUP1 mRNA is not regulated by phorbol 12-myristate 13-acetate (PMA) in HL-60 cells . Inhibition of protein synthesis by cycloheximide does not prevent the induction of VDUP1 mRNA by 1,25-dihydroxyvitamin D-3. Cycloheximide itself increases VDUP1 mRNA levels. These results suggest that the degradation of VDUP1 mRNA is either translation-dependent or regulated by a labile protein.

L4 ANSWER 9 OF 11 MEDLINE on STN
AN 93129833 MEDLINE
DN PubMed ID: 1336412
TI Oxygen toxicity.
AU Stogner S W; Payne D K
CS Department of Medicine, Louisiana State University, Shreveport.
SO Annals of pharmacotherapy, (1992 Dec) 26 (12) 1554-62. Ref: 78
Journal code: 9203131. ISSN: 1060-0280.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals; Space Life Sciences
EM 199302
ED Entered STN: 19930226
Last Updated on STN: 19930226
Entered Medline: 19930212
AB OBJECTIVE: The objective of this article is to provide an overview of the biochemistry of oxygen metabolism, including the formation of free radicals and the role of endogenous antioxidants. Pathophysiologic correlates underlying the clinical manifestations of oxygen toxicity are reviewed and management strategies are outlined. DATA SOURCES: References from basic science and clinical journals were selected from the authors' files and from a search of a computerized database of the biomedical literature. STUDY SELECTION: Articles selected for review included both historical and current literature concerning the biochemistry and pathophysiology of oxygen toxicity in animals and humans. DATA SYNTHESIS: The benefits of oxygen therapy have been known for many years; however, its potential toxicity has not been recognized until the last two decades. The lungs, the eyes, and, under certain conditions, the central nervous system are the organs most affected by prolonged exposure to hyperoxic environments. Free radical formation during cellular metabolism under hyperoxic conditions is recognized as the biochemical basis of oxygen injury to cells and organs. Endogenous antioxidants are a primary means of detoxifying reactive oxygen species and preventing hyperoxia-induced cellular damage. When this defense fails or is overwhelmed by the excessive production of hyperoxia-induced free-radical species, distinctive morphologic changes occur at the cellular level. The amount of hyperoxia required to cause cellular damage and the time course of these changes vary from species to species and from individual to individual within the same species. Age, nutritional status, presence of underlying diseases, and certain drugs may influence the development of oxygen toxicity. CONCLUSIONS: There is currently no reliably effective drug for preventing or delaying the development of oxygen toxicity in humans. Use of the lowest effective oxygen concentration, the avoidance of certain drugs, and attention to nutritional and metabolic factors remain the best means currently available to avoid or minimize oxygen toxicity. Research is continuing into more effective ways to prevent, diagnose, and treat this disorder.

L4 ANSWER 10 OF 11 MEDLINE on STN
AN 93251101 MEDLINE
DN PubMed ID: 1844886
TI Characterization of the auxin-regulated par gene from tobacco mesophyll protoplasts.
AU Takahashi Y; Kusaba M; Hiraoka Y; Nagata T
CS Department of Biology, Faculty of Science, University of Tokyo, Japan.
SO Plant journal : for cell and molecular biology, (1991 Nov) 1 (3) 327-32.

Journal code: 9207397. ISSN: 0960-7412.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Space Life Sciences
OS GENBANK-D90215; GENBANK-M29274
EM 199306
ED Entered STN: 19930618
Last Updated on STN: 19930618
Entered Medline: 19930610
AB The auxin-regulated par gene from tobacco mesophyll protoplasts was characterized in detail to deduce its possible function. An homology search of the par gene in the NBRF **databases** revealed that the par gene has homology to the stringent starvation protein (ssp) gene of Escherichia coli, which is induced under starved conditions and binds in an equimolar ratio to a holoenzyme of RNA polymerase. Hence, it is supposed that the par gene product could play a similar role to that of ssp. Although sequence homology of the par gene to the Gmhsp 26-A gene from soybean was observed, both genes were shown to respond differently to **plant** hormones and stresses. Gmhsp 26-A is induced by heat shock, 2,4-dichlorophenoxyacetic acid (2,4-D), cytokinin and abscisic acid (ABA), whereas the par gene was induced only by auxins. Furthermore, cycloheximide treatment prevents 2,4-D-mediated accumulation of Gmhsp 26-A mRNA, but not that of par mRNA. Both par and Gmhsp 26-A respond to CdCl2, but splicing of the par pre-mRNA proceeded in a normal way, whereas splicing off the Gmhsp 26-A pre-mRNA was inhibited. Hence, the par and Gmhsp 26-A genes should have a common ancestor, but have evolved in different directions. Detailed **time-course** experiments confirmed that the par gene was induced immediately after the addition of auxin and expressed upon the initiation of meristematic activity in tobacco mesophyll protoplasts. As the par gene was induced by the sole treatment of cycloheximide, it was proposed that the par gene belongs to a category of 'superinduction' genes. (ABSTRACT TRUNCATED AT 250 WORDS)

L4 ANSWER 11 OF 11 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1986:241820 BIOSIS
DN PREV198682006324; BA82:6324
TI AXONS REGENERATED THROUGH SILICONE TUBE SPLICES I. CONDUCTION PROPERTIES.
AU FIELDS R D [Reprint author]; ELLISMAN M H
CS DEP NEUROSCI, SCH MED, UNIV CALIFORNIA, SAN DIEGO, LA JOLLA, CA 92093, USA
SO Experimental Neurology, (1986) Vol. 92, No. 1, pp. 48-60.
CODEN: EXNEAC. ISSN: 0014-4886.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 7 Jun 1986
Last Updated on STN: 7 Jun 1986
AB Changes in conduction properties of axons regenerating across a 10-mm gap bridged by a silicone cuff were investigated from compound action potential responses. Compound action potentials were detected as early as 6 weeks after surgery, and were small and slowly conducted at maximum velocities of about 3 m/s. With longer regeneration time, the potentials increased in size, velocity, and complexity. Conduction velocities increased rapidly at first then slowly and asymptotically approached rates that were approximately 40% below normal after 10 months. One component of the compound action potential, the refractory period, decreased from 5 ms to near normal value after only 3 months. The time constant of excitation changed more rapidly, and after 2 months approximted values near those for conrols. The properties of axons regenerated through

silicone tube splices were comparable to those observed in axons regenerating across an epineural suture with no gaps. The **database** for the **time course** of events established here will be useful in guiding studies using the silicone cuff technique as an in situ experimental chamber for studies of regeneration and remyelination.

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L2 58 S L1 AND TIME COURSE
L3 16 S L2 AND PY<2000
L4 11 DUPLICATE REMOVE L3 (5 DUPLICATES REMOVED)

=> s time course
L5 97104 TIME COURSE

=> s l5 and multiwell
L6 14 L5 AND MULTIWELL

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L7 10 L6 AND PY<2000

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PROCESSING COMPLETED FOR L7
L8 6 DUPLICATE REMOVE L7 (4 DUPLICATES REMOVED)

=> d 1-6 bib ab

L8 ANSWER 1 OF 6 MEDLINE on STN DUPLICATE 1
AN 1998297412 MEDLINE
DN PubMed ID: 9635489
TI Transgenic nematodes as biomonitors of microwave-induced stress.
AU Daniells C; Duce I; Thomas D; Sewell P; Tattersall J; de Pomerai D
CS Department of Life Science, University of Nottingham, University Park, UK.
SO Mutation research, **(1998 Mar 13)** 399 (1) 55-64.
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199807
ED Entered STN: 19980716
Last Updated on STN: 19980716
Entered Medline: 19980702
AB Transgenic nematodes (Caenorhabditis elegans strain PC72), carrying a stress-inducible reporter gene (Escherichia coli beta-galactosidase) under the control of a C. elegans hsp16 heat-shock promoter, have been used to monitor toxicant responses both in water and soil. Because these transgenic nematodes respond both to heat and toxic chemicals by synthesising an easily detectable reporter product, they afford a useful preliminary screen for stress responses (whether thermal or non-thermal) induced by microwave radiation or other electromagnetic fields. We have used a transverse electromagnetic (TEM) cell fed from one end by a source and terminated at the other end by a matched load. Most studies were

conducted using a frequency of 750 MHz, at a nominal power setting of 27 dBm. The TEM cell was held in an incubator at 25 degrees C inside a shielded room; corresponding controls were shielded and placed in the same 25 degrees C incubator; additional baseline controls were held at 15 degrees C (worm growth temperature). Stress responses were measured in terms of beta-galactosidase (reporter) induction above control levels. The **time-course** of response to continuous microwave radiation showed significant differences from 25 degrees C controls both at 2 and 16 h, but not at 4 or 8 h. Using a 5 x 5 **multiwell** plate array exposed for 2 h, the 25 microwaved samples showed highly significant responses compared with a similar control array. The wells most strongly affected were those in the rows closest to the source, whereas the most distant row did not rise above control levels, suggesting a shadow effect. These differential responses are difficult to reconcile with general heating effects, although localised power absorption affords a possible explanation. Experiments in which the frequency and/or power settings were varied suggested a greater response at 21 than at 27 dBm, both at 750 and 300 MHz, although extremely variable responses were observed at 24 dBm and 750 MHz. Thus, lower power levels tended, if anything, to induce larger responses (with the above-mentioned exception), which is opposite to the trend anticipated for any simple heating effect. These results are reproducible and data acquisition is both rapid and simple. The evidence accrued to date suggests that microwave radiation causes measurable stress to transgenic nematodes, presumably reflecting increased levels of protein damage within cells (the common signal thought to trigger hsp gene induction). The response levels observed are comparable to those observed with moderate concentrations (ppm) of metal ions such as Zn2+ and Cu2+. We conclude that this approach deserves further and more detailed investigation, but that it has already demonstrated clear biological effects of microwave radiation in terms of the activation of cellular stress responses (hsp gene induction).

L8 ANSWER 2 OF 6 MEDLINE on STN DUPLICATE 2
AN 97288250 MEDLINE
DN PubMed ID: 9143228
TI Determination of the **time course** and extent of neurotoxicity at defined temperatures in cultured neurons using a modified **multiwell** plate fluorescence scanner.
AU Sattler R; Charlton M P; Hafner M; Tymianski M
CS Playfair Neuroscience Unit, Toronto Hospital Research Institute, Ontario, Canada.
SO Journal of cerebral blood flow and metabolism : official journal of the International Society of Cerebral Blood Flow and Metabolism, **(1997 Apr)** 17 (4) 455-63.
Journal code: 8112566. ISSN: 0271-678X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199706
ED Entered STN: 19970612
Last Updated on STN: 19970612
Entered Medline: 19970604
AB The cellular and molecular mechanisms of hypoxic/ischemic neurodegeneration are sensitive to numerous factors that modulate the **time course** and degree of neuronal death. Among such factors is hypothermia, which can dramatically protect neurons from injury. To examine and control for temperature-dependent effects, we developed a technique that provides for a high-throughput, accurate, and reproducible determination of the **time course** and degree of neurotoxicity in cultured cortical neurons at precisely defined

temperatures. We used a fluorescence **multiwell** plate scanner, modified by us to permit the control of temperature, to perform serial quantitative measurements of propidium iodide (PI) fluorescence in cortical neuronal cultures exposed to excitotoxic insults. In validating this approach, we show that these **time course** measurements correlate highly with manual counts of PI-stained cells in the same cultures ($r = 0.958$, $p < 0.0001$) and with lactate dehydrogenase release ($r = 0.964$, $p < 0.0001$). This method represents an efficient approach to mechanistic and quantitative studies of cell death as well as a high-throughput technique for screening new neuroprotective therapies in vitro.

L8 ANSWER 3 OF 6 MEDLINE on STN DUPLICATE 3
AN 97160806 MEDLINE
DN PubMed ID: 9121686
TI Use of a **multiwell** fluorescence scanner with propidium iodide to assess NMDA mediated excitotoxicity in rat cortical neuronal cultures.
AU Rudolph J G; Lemasters J J; Crews F T
CS Department of Pharmacology and Therapeutics, University of Florida, Gainesville 32610-0267, USA.
SO Neuroscience letters, **(1997 Jan 17)** 221 (2-3) 149-52.
Journal code: 7600130. ISSN: 0304-3940.
CY Ireland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199704
ED Entered STN: 19970506
Last Updated on STN: 19970506
Entered Medline: 19970418
AB Glutamate mediated excitotoxicity is a major area of experimentation due to the potential for prevention of morbidity and brain damage associated with stroke and brain trauma. We have developed a simple rapid method to study excitotoxicity in primary cortical neuronal cultures using propidium iodide (PI) fluorescence read by a **multiwell** fluorescence scanner. Transient (25 min) or continuous N-methyl-D-aspartate (NMDA) treatment led to progressive neuronal death over 24 h that was blocked by 1 microM MK-801, 10 microM ifenprodil, and 200 mM ethanol. Results with PI fluorescence were identical to those found using the lactate dehydrogenase (LDH) release and trypan blue staining assays of excitotoxicity. This method provides a simple rapid means to test the effects of drugs during glutamate excitotoxicity and to do accurate **time course** experiments of delayed neuronal death.

L8 ANSWER 4 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:548510 BIOSIS
DN PREV199699270866
TI Measurement of the **time-course** and degree of cell death in cultured cortical neurons using a **multiwell** fluoresence scanner.
AU Sattler, Rita [Reprint author]; Charlton, Milton P. [Reprint author]; Hafner, Mathias; Tymianski, Michael [Reprint author]
CS Playfair Neurosci. Unit, Univ. Toronto, Toronto, ON, Canada
SO Society for Neuroscience Abstracts, (1996) Vol. 22, No. 1-3, pp. 1909.
Meeting Info.: 26th Annual Meeting of the Society for Neuroscience. Washington, D.C., USA. November 16-21, 1996.
ISSN: 0190-5295.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English

ED Entered STN: 13 Dec 1996
Last Updated on STN: 13 Dec 1996

L8 ANSWER 5 OF 6 MEDLINE on STN DUPLICATE 4
AN 96236801 MEDLINE
DN PubMed ID: 9064285
TI Hybridoma screening for cell adhesion molecules using multiple parallel comparisons in conditions of flow.
AU Li X; Rawn J; DeCamp M M; Mentzer S J
CS Laboratory of Immunophysiology, Brigham and Women's Hospital, Boston, Massachusetts 02115, USA.
NC HL47078 (NHLBI)
SO Hybridoma, (1996 Feb) 15 (1) 43-7.
Journal code: 8202424. ISSN: 0272-457X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199703
ED Entered STN: 19970327
Last Updated on STN: 19970327
Entered Medline: 19970319
AB Cell adhesion is a complex biophysical process that plays a central role in immunophysiology. Because of the complex force-energy relationships involved, insights into the mechanism of cell adhesion largely depend on comparative measurements. In this report, we describe a comparative approach to the measurement of cell adhesion under conditions of flow. The assay system perfuses fluorescently labeled lymphocytes over a cell monolayer in commercially available **multiwell** culture plates. The fluorescently labeled cells demonstrate a reproducible flow pattern within the well. Videomicroscopic recordings of cell movement have demonstrated rolling behavior over a wide range of cell velocities. This technique permits the measurement of cell adhesion over a variety of flow velocities, **time courses**, and treatment conditions. The ability to vary treatment conditions and provide multiple parallel conditions suggests the utility of this approach in the development of monoclonal antibodies (MAb) recognizing cell adhesion molecules.

L8 ANSWER 6 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1992:187529 BIOSIS
DN PREV199293098479; BA93:98479
TI ROLE FOR CYCLIC ADENOSINE MONOPHOSPHATE IN THE SYNERGISTIC INTERACTION BETWEEN OXYTOCIN AND CORTICOTROPHIN-RELEASING FACTOR IN ISOLATED HUMAN GESTATIONAL MYOMETRIUM.
AU QUARTERO H W P [Reprint author]; SRIVATSA G; GILLHAM B
CS DEP OSTET GYNECOL, ACADEMIC HOSP ROTTERDAM DIJKZIGT, ERASMUS UNIV ROTTERDAM, DR MOLEWATERPLEIN 40, 3015 GD ROTTERDAM, NETH
SO Clinical Endocrinology, (1992) Vol. 36, No. 2, pp. 141-145.
CODEN: CLECAP. ISSN: 0300-0664.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 13 Apr 1992
Last Updated on STN: 1 Jun 1992
AB OBJECTIVE: We wished to investigate the role of cAMP in the synergistic effect of corticotrophin-releasing factor and oxytocin on human myometrial contractility. DESIGN: Isolated human gestation myometrium obtained from Caesarean sections at term was studied in vitro. Static incubation techniques as well as tension recordings were applied to the tissue obtained. PATIENTS: The subjects were healthy pregnant women undergoing lower segment Caesarean section at term, prior to labour. MEASUREMENTS:

Specimens obtained were immediately dissected into small strips and either incubated in multiwell trays (strip weight 2.75 mg) or superfused and used for tension recordings (strip weight 2.00 mg). cAMP accumulation was measured after incubation wth oxytocin (0.1-10 nM), corticotrophin-releasing factor (1 nM) or a combination of both peptides. Tension generated by the muscle strips was recorded isometrically and response to oxytocin (0.01-10 nM), corticotrophin-releasing factor (1 nM) and forskolin (10 nM) expressed in force per gram wet tissue (N/g). RESULTS: Oxytocin (0.1 nM) causes a statistically significant dose-related decrease in cAMP when combined with 1 nM corticotrophin-releasing factor ($P < 0.001$), as compared with cAMP stimulation by corticotrophin-releasing factor alone. Time course studies suggest a maximal effect at 1 minute. The hypothesis that an intracellular reduction of cAMP is a prerequisite for the synergistic response in contraction force was tested with tension recordings. Prevention of a decrease in cAMP in the tissue by addition of 10 nM forskolin to the superfusate abolished the potentiation between oxytocin and corticotrophin-releasing factor. CONCLUSIONS: These results indicate that a fall cAMP concentration plays a vital mediating role in the synergistic interaction between oxytocin and corticotrophin-releasing factor.

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=> s database and labortory
L1            0 DATABASE AND LABORTORY

=> s database and laboratory
L2         7660 DATABASE AND LABORATORY

=> s l2 and time course
L3            6 L2 AND TIME COURSE

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L4   ANSWER 1 OF 6  BIOSIS  COPYRIGHT (c) 2004 The Thomson Corporation.  on STN
AN   2004:284392  BIOSIS
DN   PREV200400288837
TI   SPI: a tool for incorporating gene expression data into a four-dimensional
     database of Caenorhabditis elegans embryogenesis.
AU   Minakuchi, Yohei; Ito, Masahiro; Kohara, Yuji [Reprint Author]
CS   Genome Biol Lab, Natl Inst Genet, 1111 Yata, Shizuoka, 4118540, Japan
     ykohara@lab.nig.ac.jp
SO   Bioinformatics (Oxford), (May 1 2004) Vol. 20, No. 7, pp. 1097-1109.
     print.
     ISSN: 1367-4803.
DT   Article
LA   English
ED   Entered STN: 16 Jun 2004
     Last Updated on STN: 16 Jun 2004
AB   Motivation: A comprehensive gene expression database is
     essential for computer modeling and simulation of biological phenomena,
     including development. Development is a four-dimensional (4D; 3D
     structure and time course) phenomenon. We are
     constructing a 4D database of gene expression for the early
     embryogenesis of the nematode Caenorhabditis elegans. As a framework of
     the 4D database, we have constructed computer graphics (CG),
     into which we will incorporate the expression data of a number of genes at
     the subcellular level. However, the assignment of 3D distribution of gene
     products (protein, mRNA), of embryos at various developmental stages, is
     both difficult and tedious. We need to automate this process. For this
     purpose, we developed a new system, named SPI after superimposing
     fluorescent confocal microscopic data onto a CG framework. Results: The
     scheme of this system comprises the following: (1) acquirement of serial
     sections (40 slices) of fluorescent confocal images of three colors
     (4',6'-diamino-2-phenylindole (DAPI) for nuclei, indodicarbocyanine (Cy-3)
     for the internal marker, which is a germline-specific protein POS-1 and
     indocarbocyanine (Cy-5) for the gene product to be examined); (2)
     identification of several features of the stained embryos, such as
     contour, developmental stage and position of the internal marker; (3)
     selection of CG images of the corresponding stage for template matching;
     (4) superimposition of serial sections onto the CG; (5) assignment of the
     position of superimposed gene products. The Snakes algorithm identified
     the embryo contour. The detection accuracy of embryo contours was 92.1%
     when applied to 2- to 28-cell-stage embryos. The accuracy of the
     developmental stage prediction method was 81.2% for 2- to 8-cell-stage
     embryos. We manually judged only the later stage embryos because the
     accuracy for embryos at the later stages was unsatisfactory due to
     experimental noise effects. Finally, our system chose the optimal CG and
     performed the superposition and assignment of gene product distribution.
     We established an initial 4D gene expression database with 56
     maternal gene products.

L4   ANSWER 2 OF 6  BIOSIS  COPYRIGHT (c) 2004 The Thomson Corporation.  on STN
AN   2004:90572  BIOSIS
DN   PREV200400093380
TI   Identification of temporal patterns of gene expression in the uteri of
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immature, ovariectomized mice following exposure to ethynylestradiol.
AU Fertuck, H. C.; Eckel, J. E.; Gennings, C.; Zacharewski, T. R. [Reprint Author]
CS Dept. of Biochemistry and Molecular Biology, Michigan State Univ., Wilson Road, Biochemistry Bldg., East Lansing, MI, 48824-1319, USA tzachare@msu.edu
SO Physiological Genomics, (January 2004) Vol. 15, pp. 127-141. print. ISSN: 1094-8341 (ISSN print).
DT Article
LA English
ED Entered STN: 11 Feb 2004
Last Updated on STN: 11 Feb 2004
AB Estrogen induction of uterine wet weight provides an excellent model to investigate relationships between changes in global gene expression and well-characterized physiological responses. In this study, **time course** microarray GeneChip data were analyzed using a novel approach to identify temporal changes in uterine gene expression following treatment of immature ovariectomized C57BL/6 mice with 0.1 mg/kg 17alpha-ethynylestradiol. Functional gene annotation information from public **databases** facilitated the association of changes in gene expression with physiological outcomes, which allowed detailed mechanistic inferences to be drawn regarding cell cycle control and proliferation, transcription and translation, structural tissue remodeling, and immunologic responses. These systematic approaches confirm previously established responses, identify novel estrogen-regulated transcriptional effects, and disclose the coordinated activation of multiple modes of action that support the uterotrophic response elicited by estrogen. In particular, it was possible to elucidate the physiological significance of the dramatic induction of arginase, a classic estrogenic response, by elucidating its mechanistic relevance and delineating the role of arginine and ornithine utilization in the estrogen-stimulated induction of uterine wet weight.

L4 ANSWER 3 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2004:348890 BIOSIS
DN PREV200400350291
TI Ozone-induced acute pulmonary injury in inbred mouse strains.
AU Savov, Jordan D. [Reprint Author]; Whitehead, Gregory S.; Wang, Jianme; Liao, Guochun; Usuka, Jonathan; Peltz, Gary; Foster, W. Michael; Schwartz, David A.
CS Med CtrDiv Pulm Allergy and Crit Care MedDept Med, Duke Univ, POB 2629, Durham, NC, 27710, USA jsavov@duke.edu
SO American Journal of Respiratory Cell and Molecular Biology, (July 2004) Vol. 31, No. 1, pp. 69-77. print. ISSN: 1044-1549 (ISSN print).
DT Article
LA English
ED Entered STN: 18 Aug 2004
Last Updated on STN: 18 Aug 2004
AB To determine if host factors influence the **time course** and extent of lung injury after acute inhalation of ozone (03), we evaluated the physiologic and biologic response of nine genetically diverse inbred strains of mice (C57BL/6J, 129/Svlm, BTBR, BALB/cJ, DBA/2J, A/J, FVB/NJ, CAST/Ei, and C3H/HeJ) exposed to 03 (2.0 ppm x 3 h). Whole lung lavage determined that 129/Svlm, BTBR, DBA/2J, and FVB/NJ had a peak increase in polymorphonuclear cells (PMNs) at 6 h, whereas C57BL/6J and CAST/Ei had a peak increase at 24 h after exposure; airway PMNs were minimally elevated in A/J and C3H/HeJ; BALB/cJ had a predominant lymphocytic influx. Interleukin-6 concentration in the lavage fluid was associated with the influx of PMNs, whereas the total protein in the lavage fluid did not always correlate with lavage cellularity. Respiratory responses were monitored using whole body plethysmography and enhanced pause index. C57BL/6J, BALB/cJ, 129/Svlm, and BTBR were highly sensitive to 03 and exhibited significant increases in enhanced pause to methacholine aerosol stimulation at 6 and 24 h after exposure to 03. In contrast, DBA/2J, A/J, FVB/NJ, CAST/Ei, and C3H/HeJ strains had demonstrated increases in sensitivity to MCh at 6 h after exposure, but responses had returned to near baseline by 24 h after exposure to 03.

Epithelial cell proliferation as assessed by proliferating cell nuclear antigen staining was evident at 24 h after exposure to O3. C57BL/6J and A/J showed 4% proliferating cell nuclear antigen-positive cells; 129/Svlm, DBA/2J, and FVB/NJ had 1-3%; and BTBR, BALB/cJ, CAST/Ei, and C3H/HeJ had < 1%. Phenotypic measurements in six inbred strains were used for an in silico genome analysis based on the Roche mouse **database**. Consistent loci on chromosomes 1, 7, and 15 were among those identified to have a significant association with the phenotypes studied. In aggregate, our approach has identified O3-resistant (C3H/HeJ and A/J) and -vulnerable (C57BL/6J and 129/Svlm) strains of mice, and determined novel genomic loci, suggesting a clear genetic basis for the lung response to inhaled O3.

L4 ANSWER 4 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2003:316321 BIOSIS
DN PREV200300316321
TI Proteomics approach to identify wound-response related proteins from rice leaf sheath.
AU Shen, Shihua [Reprint Author]; Jing, Yuxiang; Kuang, Tingyun
CS Institute of Botany, Chinese Academy of Sciences, Xiangshan, Beijing, 100093, China
shshen@ns.ibcas.ac.cn
SO Proteomics, (April 2003) Vol. 3, No. 4, pp. 527-535. print.
ISSN: 1615-9853 (ISSN print).
DT Article
LA English
ED Entered STN: 9 Jul 2003
Last Updated on STN: 9 Jul 2003
AB In order to avoid the complex conditions of the intact plant for simple analysis of proteins in wound-response stress, we used the detached rice leaf sheath which is a very active part of the rice seedling. Proteins were extracted from rice leaf sheath at 0, 12, 24, 48 h after cutting and separated by two-dimensional (2-D) polyacrylamide gel electrophoresis. Changes in differentially displayed proteins were found in leaf sheaths after cutting in the 0-48 h **time course**. Ten proteins were up-regulated, while 19 proteins were down-regulated compared with those on the four 2-D gels. Among them, 14 proteins were analyzed by N-terminal, or internal amino acid sequence. The clear functions of nine proteins could be identified. Six proteins did not yield amino acid sequence information due to their blocked N-termini. Furthermore, 11 proteins were determined by matrix-assisted laser desorption/ionization-time of flight mass spectrometry, and identified protein **database** matching. It was shown that the down-regulated proteins were calreticulin (nos. 5,6), histone H1 (number 15) and hemoglobin (number 17), putative peroxidase (number 19); the up-regulated proteins were Bowman-Birk trypsin inhibitor (number 23), putative receptor-like protein kinase (nos. 24, 25), calmodulin-related protein (number 26), small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (number 27), mannose-binding rice lectin (nos. 28, 29). Among all the above proteins, four (nos. 23, 24, 25, 26) have been confirmed to be wound-response proteins. The others cannot be excluded as also being related to wound-responses, such as the signal transduction-related proteins (nos. 5, 6), photosynthesis-related protein (number 27), and stress-response proteins (nos. 19, 28, 29). This is the first time protein changes in response to wounding in rice leaf sheath have been shown.

L4 ANSWER 5 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2003:513898 BIOSIS
DN PREV200300516282
TI Toxicity classification from metabonomic data using a density superposition approach: 'CLOUDS'.
AU Ebbels, Tim [Reprint Author]; Keun, Hector; Beckonert, Olaf; Antti, Henrik; Bollard, Mary; Holmes, Elaine; Lindon, John; Nicholson, Jeremy
CS Biological Chemistry, Biomedical Sciences Division, Faculty of Medicine, Imperial College of Science, Technology and Medicine, South Kensington, Sir Alexander Fleming Building, London, SW7 2AZ, UK
t.ebbels@ic.ac.uk
SO Analytica Chimica Acta, (25 August 2003) Vol. 490, No. 1-2, pp. 109-122. print.

ISSN: 0003-2670 (ISSN print).
DT Article
LA English
ED Entered STN: 5 Nov 2003
Last Updated on STN: 5 Nov 2003
AB Predicting and avoiding the potential toxicity of candidate drugs is of fundamental importance to the pharmaceutical industry. The consortium for metabonomic toxicology (COMET) project aims to construct **databases** and metabolic models of drug toxicity using ca. 100,000 600 MHz 1H NMR spectra of biofluids from **laboratory** rats and mice treated with model toxic compounds. Chemometric methods are being used to characterise the time-related and dose-specific effects of toxins on the endogenous metabolite profiles. Here we present a probabilistic approach to the classification of a large data set of COMET samples using Classification Of Unknowns by Density Superposition (CLOUDS), a novel non-neural implementation of a classification technique developed from probabilistic neural networks. NMR spectra of urine from rats from 19 different treatment groups, collected over 8 days, were processed to produce a data matrix with 2844 samples and 205 spectral variables. The spectra were normalised to account for gross concentration differences in the urine and regions corresponding to non-endogenous metabolites (0.4% of the data) were treated as missing values. Modeling the data according to organ of effect (control, liver, kidney or other organ), with a 50/50 train/test set split, over 90% of the test samples were classified as belonging to the correct group. In particular, samples from liver and kidney treatments were classified with 77 and 90% success, respectively, with only a 2% misclassification rate between these classes. Further analysis of the data, counting each of the 19 treatment groups as separate classes, resulted in a mean success rate across groups of 74%. Finally, as a severe test, the data were split into 88 classes, each representing a particular toxin at a particular time point. Fifty-four percent of the spectra from non-control samples were classified correctly, particularly successful when compared to the null success rate of apprx1% expected from random class assignment. The CLOUDS technique has advantages when modelling complex multi-dimensional distributions, giving a probabilistic rather than absolute class description of the data and is particularly amenable to inclusion of prior knowledge such as uncertainties in the data descriptors. This work shows that it is possible to construct viable and informative models of metabonomic data using the CLOUDS methodology, delineating the whole **time course** of toxicity. These models will be useful in building hybrid expert systems for predicting toxicology, which are the ultimate goal of the COMET project.

L4 ANSWER 6 OF 6 MEDLINE on STN
AN 2000510965 MEDLINE
DN PubMed ID: 11064595
TI Exploratory analysis of elevated C-reactive protein without leukocytosis from the clinical **laboratory database**.
AU Ishida H; Ichihara K; Matsuda N
CS Department of Clinical Pathology, Kawasaki Medical School, Kurashiki.
SO Rinsho byori. Japanese journal of clinical pathology, (2000 Aug) 48 (8) 722-9.
Journal code: 2984781R. ISSN: 0047-1860.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA Japanese
FS Priority Journals
EM 200012
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001220
AB We studied the characteristics of admitted patients who showed discrepancy between C-reactive protein(CRP) and white blood cell count(WBC). We extracted those patients from our **laboratory** information system by two criteria: WBC is less than 9500/microliter and either(1) CRP is more than 5.0 mg/dl, or(2) the pair of CRP and WBC is out of 95% confidence ellipse. We found 346 and 90 cases by the two criteria, respectively. They consisted of a variety of diseases, prevalent were such as pneumonia, rheumatoid arthritis, malignant lymphoma,

post-operative state and so on by either criterion. There was predominance of elderly patients as a whole. The analysis of individual **time courses** revealed that WBC did not change in parallel with CRP in patients with rheumatoid arthritis and malignant lymphoma, while they paralleled in those with infectious diseases and post-operation states. The elevation of WBC in some patients might have been overlooked since WBC was not always to be ordered together with CRP. We need a prospective study to closely analyze serial relationship between CRP and WBC for factors leading to the discovery.

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     FILE 'MEDLINE, BIOSIS' ENTERED AT 17:18:45 ON 29 SEP 2004
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L2          7660 S DATABASE AND LABORATORY
L3             6 S L2 AND TIME COURSE
L4             6 DUPLICATE REMOVE L3 (0 DUPLICATES REMOVED)

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L5           862 L2 AND EXPERIMENT?

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L6           276 L5 AND (CELL OR CULTURE OR PLANT)

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L7            60 L6 AND PY<2000

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L8            45 DUPLICATE REMOVE L7 (15 DUPLICATES REMOVED)

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L8   ANSWER 1 OF 45     MEDLINE on STN                    DUPLICATE 1
AN   2000077531     MEDLINE
DN   PubMed ID: 10612284
TI   The microbial proteome database--an automated laboratory
     catalogue for monitoring protein expression in bacteria.
AU   Cordwell S J; Nouwens A S; Verrills N M; McPherson J C; Hains P G; Van Dyk
     D D; Walsh B J
CS   Australian Proteome Analysis Facility, Macquarie University..
     scordwell@proteome.org.au
SO   Electrophoresis, (1999 Dec) 20 (18) 3580-8.
     Journal code: 8204476. ISSN: 0173-0835.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200001
ED   Entered STN: 20000114
     Last Updated on STN: 20000114
     Entered Medline: 20000105
AB   Laboratories devoted to high-throughput characterisation of
     purified proteins arrayed via two-dimensional (2-D) gel electrophoresis
     face an arduous task in maintaining a centralised and constantly evolving
     record of information relating to the characterisation of proteins and
     their responses following biological challenges. The Microbial Proteome
     Database (MPD) has been conceived as an in-house resource for
     complementing the plethora of genomic databases available for
     such organisms. The database utilises commercially available
     software to provide an electronic 'lab book' of information obtained daily
     from 2-D electrophoresis gels, image analysis packages, protein
     characterisation methodologies, and biological experimentation.
     The MPD begins from a single 2-D gel image (a 2-D 'reference map') with
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clickable spots that link to a 'protein catalogue' (ProtCat) with spot information including protein identity, changes in expression determined under **experimental** conditions, cellular location, mass, and pI. The entry for each protein then contains further links to gel images corresponding to the presence of the particular protein within different subproteomes (as defined by the pH of narrow- and wide-range immobilised pH gradients or from differential extraction methods used to determine the location of the protein within a functional **cell**). The **database** currently contains information from strains of three microbial species (Escherichia coil, Pseudomonas aeruginosa and Staphylococcus aureus) and 32 master gel images. The rapid accessibility of information obtained from microbial proteomes is an essential step towards the integrated analysis of these organisms at the gene, transcript, protein and functional levels and will aid in reducing turnaround times between sample preparation and the discovery of molecules of biological significance.

L8 ANSWER 2 OF 45 MEDLINE on STN
AN 1999352964 MEDLINE
DN PubMed ID: 10424165
TI Microorganism identification by mass spectrometry and protein **database** searches.
AU Demirev P A; Ho Y P; Ryzhov V; Fenselau C
CS Department of Chemistry and Biochemistry, University of Maryland, College Park 20742, USA.
SO Analytical chemistry, **(1999 Jul 15)** 71 (14) 2732-8.
Journal code: 0370536. ISSN: 0003-2700.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199910
ED Entered STN: 19991026
Last Updated on STN: 19991026
Entered Medline: 19991008
AB A method for rapid identification of microorganisms is presented, which exploits the wealth of information contained in prokaryotic genome and protein sequence **databases**. The method is based on determining the masses of a set of ions by MALDI TOF mass spectrometry of intact or treated **cells**. Subsequent correlation of each ion in the set to a protein, along with the organismic source of the protein, is performed by searching an Internet-accessible protein **database**. Convoluting the lists for all ions and ranking the organisms corresponding to matched ions results in the identification of the microorganism. The method has been successfully demonstrated on B. subtilis and E. coli, two organisms with completely sequenced genomes. The method has been also tested for identification from mass spectra of mixtures of microorganisms, from spectra of an organism at different growth stages, and from spectra originating at other **laboratories**. **Experimental** factors such as MALDI matrix preparation, spectral reproducibility, contaminants, mass range, and measurement accuracy on the **database** search procedure are addressed too. The proposed method has several advantages over other MS methods for microorganism identification.

L8 ANSWER 3 OF 45 MEDLINE on STN
AN 1999178942 MEDLINE
DN PubMed ID: 10077564
TI Troponin I is present in human cartilage and inhibits angiogenesis.
AU Moses M A; Wiederschain D; Wu I; Fernandez C A; Ghazizadeh V; Lane W S; Flynn E; Sytkowski A; Tao T; Langer R
CS Laboratory for Surgical Research, The Children's Hospital, Boston, MA 02115, USA.. moses_m@A1.tch.harvard.edu
NC AR21673 (NIAMS)
SO Proceedings of the National Academy of Sciences of the United States of America, **(1999 Mar 16)** 96 (6) 2645-50.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
EM 199905
ED Entered STN: 19990601
Last Updated on STN: 19990601
Entered Medline: 19990520
AB Cartilage is an avascular and relatively tumor-resistant tissue. Work from a number of **laboratories**, including our own, has demonstrated that cartilage is an enriched source of endogenous inhibitors of angiogenesis. In the course of a study designed to identify novel cartilage-derived inhibitors of new capillary growth, we have purified an inhibitory protein that was identified by peptide microsequencing and protein **database** analysis as troponin I (TnI). TnI is a subunit of the troponin complex (troponin-C and troponin-T being the other two), which, along with tropomyosin, is responsible for the calcium-dependent regulation of striated muscle contraction; independently, TnI is capable of inhibiting actomyosin ATPase. Because troponin has never previously been reported to be present in cartilage, we have cloned and expressed the cDNA of human cartilage TnI, purified this protein to apparent homogeneity, and demonstrated that it is a potent and specific inhibitor of angiogenesis in vivo and in vitro, as well as of tumor metastasis in vivo.

L8 ANSWER 4 OF 45 MEDLINE on STN
AN 1999416746 MEDLINE
DN PubMed ID: 10490383
TI Microbial genomes.
AU Pallen M J
CS Department of Medical Microbiology, St Bartholomew's and the Royal London School of Medicine and Dentistry, West Smithfield, London, UK.. m.pallen@qmw.ac.uk
SO Molecular microbiology, **(1999 Jun)** 32 (5) 907-12.
Journal code: 8712028. ISSN: 0950-382X.
CY ENGLAND: United Kingdom
DT Conference; Conference Article; (CONGRESSES)
LA English
FS Priority Journals
EM 199909
ED Entered STN: 19990925
Last Updated on STN: 19990925
Entered Medline: 19990915
AB Microbial genome sequencing is driven by the need to understand and control pathogens and to exploit extremophiles and their enzymes in bioremediation and industry. It is hard for the traditional bacteriologist to grasp the scale and pace of the venture. Around two dozen microbial genomes have now been completed and, within a decade, genomes from every significant species of bacterial pathogen of humans, animals and **plants** will have been sequenced. Indeed, we will often have more than one sequence from a species or genus--for example, we already have sequences from two strains of Helicobacter pylori, from two strains of Mycobacterium tuberculosis and from three species of Pyrococcus. However, genome sequencing risks becoming expensive molecular stamp-collecting without the tools to mine the data and fuel hypothesis-driven **laboratory**-based research. Bioinformatics, twinned with the new **experimental** approaches forming functional genomics', provides some of the needed tools. Nonetheless, there will be an increasing need for us to explore the detailed implications of genomic findings. Microbial genome sequencing thus represents not a threat, but an exciting opportunity for molecular microbiologists.

L8 ANSWER 5 OF 45 MEDLINE on STN DUPLICATE 2
AN 2000023637 MEDLINE
DN PubMed ID: 10560981
TI Seasonal variations and age-related changes in human sperm count, motility, motion parameters, morphology, and white blood **cell** concentration.
AU Centola G M; Eberly S
CS Department of Obstetrics and Gynecology, University of Rochester Medical Center, New York 14642, USA.. grace_centola@urmc.rochester.edu
SO Fertility and sterility, **(1999 Nov)** 72 (5) 803-8.

Journal code: 0372772. ISSN: 0015-0282.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199912
ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991207
AB OBJECTIVE: To determine the presence of any seasonal variations and age-related changes in sperm parameters in andrology patients and fertile donors. DESIGN: Retrospective analysis. SETTING: University medical center andrology **laboratory**. PATIENT(S): The **database** of 2,065 semen analyses was retrospectively reviewed for the period of March 1, 1996, to October 31, 1998. INTERVENTION(S): None. MAIN OUTCOME MEASURES(S): The sperm count, motility, motile count, progressive straightline velocity, and percentage of rapid sperm were determined with the Hamilton-Thorne IVOS analyzer with standard setup parameters. RESULT(S): There were no significant seasonal differences in the patient's volume, sperm count, motility, motile count, whereas the percentage of rapid sperm and progressive straightline velocity were significantly lower in the spring. Correlation analysis of patient semen parameters versus age implied that as age increases there is a tendency for these semen parameters to decrease, whereas percent tail defects showed a significant positive correlation with age. CONCLUSION(S): Age-adjusted analyses of seasonal variations in andrology patient semen parameters showed significant seasonal variation in the percentage rapid motile sperm and straightline velocity, as well as the percent tail defects, percent immature sperm, and the percent tapered sperm. Such seasonal variations might prove to be clinically relevant and important when designing **experimental** protocols.

L8 ANSWER 6 OF 45 MEDLINE on STN
AN 1999383687 MEDLINE
DN PubMed ID: 10456687
TI Differential gene expression in drug metabolism and toxicology: practicalities, problems and potential.
AU Rockett J C; Esdaile D J; Gibson G G
CS Molecular Toxicology Laboratory, School of Biological Sciences, University of Surrey, Guildford, UK.
SO Xenobiotica; fate of foreign compounds in biological systems, **(1999 Jul)** 29 (7) 655-91. Ref: 123
Journal code: 1306665. ISSN: 0049-8254.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199910
ED Entered STN: 19991026
Last Updated on STN: 19991026
Entered Medline: 19991012
AB 1. An important feature of the work of many molecular biologists is identifying which genes are switched on and off in a **cell** under different environmental conditions or subsequent to xenobiotic challenge. Such information has many uses, including the deciphering of molecular pathways and facilitating the development of new **experimental** and diagnostic procedures. However, the student of gene hunting should be forgiven for perhaps becoming confused by the mountain of information available as there appears to be almost as many methods of discovering differentially expressed genes as there are research groups using the technique. 2. The aim of this review was to clarify the main methods of differential gene expression analysis and the mechanistic principles underlying them. Also included is a discussion on some of the practical aspects of using this technique. Emphasis is placed on the so-called 'open' systems, which require no prior knowledge of the genes contained within the study model. Whilst these will eventually be replaced by 'closed' systems in the study of human, mouse and other commonly studied

laboratory animals, they will remain a powerful tool for those examining less fashionable models. 3. The use of suppression-PCR subtractive hybridization is exemplified in the identification of up- and down-regulated genes in rat liver following exposure to phenobarbital, a well-known inducer of the drug metabolizing enzymes. 4. Differential gene display provides a coherent platform for building libraries and microchip arrays of 'gene fingerprints' characteristic of known enzyme inducers and xenobiotic toxicants, which may be interrogated subsequently for the identification and characterization of xenobiotics of unknown biological properties.

L8 ANSWER 7 OF 45 MEDLINE on STN DUPLICATE 3
AN 1999448268 MEDLINE
DN PubMed ID: 10517999
TI The HUman MicroNucleus Project--An international collaborative study on the use of the micronucleus technique for measuring DNA damage in humans.
AU Fenech M; Holland N; Chang W P; Zeiger E; Bonassi S
CS CSIRO Human Nutrition, Gouger Street, P.O. Box 10041, Adelaide, Australia.. michael.fenech@dhn.csiro.au
SO Mutation research, **(1999 Jul 16)** 428 (1-2) 271-83. Ref: 73
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199911
ED Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991108
AB The International Collaborative Project on Micronucleus Frequency in Human Populations (HUMN) was organized to collect data on micronucleus (MN) frequencies in different human populations and different **cell** types. The test procedures considered by this project are assays using human lymphocytes (cytokinesis-block method), exfoliated epithelial **cells**, and other **cell** types. Data (including descriptions of the populations monitored, detailed test protocols, and test results) are being obtained from a large number of **laboratories** throughout the world and are being entered into a unified **database**. The information will be used to: (1) determine the extent of variation of 'normal' values for different **laboratories** and the influence of other factors potentially affecting baseline MN frequency, e.g., age, gender and life-style; (2) provide information on the effect of **experimental** protocol variations on MN frequency measurements; (3) design and test optimal protocols for the different **cell** types; and (4) determine the extent to which MN frequency is a valid biomarker of ageing and risk for diseases such as cancer.

L8 ANSWER 8 OF 45 MEDLINE on STN DUPLICATE 4
AN 2000020725 MEDLINE
DN PubMed ID: 10529348
TI Zinc finger peptides for the regulation of gene expression.
AU Klug A
CS Medical Research Council Laboratory of Molecular Biology, Hills Road, Cambridge, CB2 2QH, UK.
SO Journal of molecular biology, **(1999 Oct 22)** 293 (2) 215-8. Ref: 19
Journal code: 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199911
ED Entered STN: 20000111
Last Updated on STN: 20000111

Entered Medline: 19991119

AB Zinc fingers are small DNA-binding peptide motifs that were discovered in this **laboratory**. These motifs can be used as modular building blocks for the construction of larger protein domains that recognise and bind to specific DNA sequences. Phage display has been used to create a large library of different zinc fingers from which selections were made for binding to a given DNA sequence. From this **database** there have been elucidated elements of recognition rules that relate the amino acid sequence of a finger to its preferred DNA binding site. Control of gene expression using designed zinc finger peptides has been demonstrated by the specific inhibition of an oncogene mouse **cell** line and also by switching on genes in expression plasmids. These **experiments** demonstrate that zinc finger DNA-binding domains can be engineered de novo to recognise given DNA sequences. Five to six individual zinc fingers linked together would recognise a DNA sequence 15-18 bp in length, sufficiently long to constitute a rare address in the human genome. By adding functional groups to the engineered DNA-binding domains, e.g. silencing domains, novel transcription factors can be generated to up- or downregulate expression of a target gene. Among potential applications are the repression of oncogene expression and the disruption of the reproductive cycle of virus infection.

L8 ANSWER 9 OF 45 MEDLINE on STN DUPLICATE 5
AN 2000101927 MEDLINE
DN PubMed ID: 10635988
TI Validation of the human T-lymphocyte cloning assay--ring test report from the EU concerted action on HPRT mutation (EUCAHM).
CM Comment in: Mutat Res. 1999 Dec 17;431(2):vii-xii. PubMed ID: 10635983
AU Hou S M; Van Dam F J; de Zwart F; Warnock C; Mognato M; Turner J; Podlutskaja N; Podlutsky A; Becker R; Barnett Y; Barnett C R; Celotti L; Davies M; Huttner E; Lambert B; Tates A D
CS Karolinska Institute, Department of Biosciences, CNT/NOVUM, Huddinge, Sweden.. saimei.hou@csb.ki.se
SO Mutation research, **(1999 Dec 17)** 431 (2) 211-21.
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
(MULTICENTER STUDY)
LA English
FS Priority Journals
EM 200002
ED Entered STN: 20000209
Last Updated on STN: 20020125
Entered Medline: 20000203

AB The T-**cell** cloning assay, which enables the enumeration and molecular analysis of 6-thioguanine resistant (HPRT-negative) mutant T-**cells**, has been extensively used for studying human somatic gene mutation in vivo. However, large inter-**laboratory** variations in the HPRT mutant frequency (MF) call for further investigation of inter-**laboratory** differences in the **experimental** methodology, and development of an optimal but easy uniform cloning protocol. As part of the EU Concerted Action on HPRT Mutation (EUCAHM), we have carried out two Ring tests for the T-**cell** cloning assay. For each test, duplicate and coded samples from three buffy coats were distributed to five **laboratories** for determination of MF using six different protocols. The results indicated a good agreement between split samples within each **laboratory**. However, both the cloning efficiencies (CEs) and MFs measured for the same blood donors showed substantial inter-**laboratory** variations. Also, different medium compositions used in one and the same **laboratory** resulted in a remarkable difference in the level of MF. A uniform operating protocol (UOP) was proposed and compared with the traditional protocols in the second Ring test. The UOP (preincubation) increased the CE in **laboratories** traditionally using preincubation, but decreased the CE in **laboratories** traditionally using priming. Adjusted for donor, use of different protocols contributed significantly to the overall variation in lnCE ($P = 0.0004$) and lnMF ($P = 0.03$), but there was no significant **laboratory** effect on the lnCE ($P = 0.38$) or lnMF ($P = 0.14$)

produced by the UOP alone. Finally, a simplified version of the UOP using the serum-free medium X-Vivo 10 and PMA was tested in one **laboratory**, and found to produce a considerable increase in CE. This modified UOP needs to be further evaluated in order to be used for future **databases** on HPRT MFs in various populations.

L8 ANSWER 10 OF 45 MEDLINE on STN DUPLICATE 6
AN 2000101926 MEDLINE
DN PubMed ID: 10635987
TI New approaches to understanding p53 gene tumor mutation spectra.
CM Comment in: Mutat Res. 1999 Dec 17;431(2):vii-xii. PubMed ID: 10635983
AU Hollstein M; Hergenhahn M; Yang Q; Bartsch H; Wang Z Q; Hainaut P
CS Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany..
m.hollstein@dkfz-heidelberg.de
NC R01 CA 79493-01 (NCI)
SO Mutation research, **(1999 Dec 17)** 431 (2) 199-209. Ref: 83
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200002
ED Entered STN: 20000209
Last Updated on STN: 20000209
Entered Medline: 20000203
AB The first p53 gene mutation arising in a human tumor was described a decade ago by Baker et al. [S.J. Baker, E.R. Fearon, J.M. Nigro, S.R. Hamilton, A.C. Preisinger, J.M. Jessup, P. van Tuinen, D.H. Ledbetter, D.F. Barker, Y. Nakamura, R. White, B. Vogelstein, Chromosome 17 deletions and p53 gene mutations in colorectal carcinomas, Science 244 (1989) 217-221]. There are now over 10,000 mutations extracted from the published literature in the IARC **database** of human p53 tumor mutations [P. Hainaut, T. Hernandez, A. Robinson, P. Rodriguez-Tome, T. Flores, M. Hollstein, C.C. Harris, R. Montesano, IARC **database** of p53 gene mutations in human tumors and **cell** lines: updated compilation, revised formats and new visualization tools, Nucleic Acids Res. 26 (1998) 205-213; Version R3, January 1999]. A large and diverse collection of tumor mutations in cancer patients provides important information on the nature of environmental factors or biological processes that are important causes of human gene mutation, since xenobiotic mutagens as well as endogenous mechanisms of genetic change produce characteristic types of patterns in target DNA [J.H. Miller, Mutational specificity in bacteria, Annu. Rev. Genet. 17 (1983) 215-238; T. Lindahl, Instability and decay of the primary structure of DNA, Nature 362 (1993) 709-715; S.P. Hussain, C.C. Harris, Molecular epidemiology of human cancer: contribution of mutation spectra studies of tumor suppressor genes, Cancer Res. 58 (1998) 4023-4037; P. Hainaut, M. Hollstein, p53 and human cancer: the first ten thousand mutations, Adv. Cancer Res. 2000]. P53 gene mutations in cancers can be compared to point mutation spectra at the HPRT locus of human lymphocytes from patients or healthy individuals with known exposure histories, and accumulated data indicate that mutation patterns at the two loci share certain general features. Hypotheses regarding specific cancer risk factors can be tested by comparing p53 tumor mutations typical of a defined patient group against mutations generated **experimentally** in rodents or in prokaryotic and eukaryotic **cells** in vitro. Refinements of this approach to hypothesis testing are being explored that employ human p53 sequences introduced artificially into **experimental** organisms used in **laboratory** mutagenesis assays. P53-specific **laboratory** models, combined with DNA microchips designed for high through-put mutation screening promise to unmask information currently hidden in the compilation of human tumor p53 mutations.

=> d his

(FILE 'HOME' ENTERED AT 17:18:33 ON 29 SEP 2004)

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     FILE 'MEDLINE, BIOSIS' ENTERED AT 17:18:45 ON 29 SEP 2004
L1             0 S DATABASE AND LABORTORY
L2          7660 S DATABASE AND LABORATORY
L3             6 S L2 AND TIME COURSE
L4             6 DUPLICATE REMOVE L3 (0 DUPLICATES REMOVED)
L5           862 S L2 AND EXPERIMENT?
L6           276 S L5 AND (CELL OR CULTURE OR PLANT)
L7            60 S L6 AND PY<2000
L8            45 DUPLICATE REMOVE L7 (15 DUPLICATES REMOVED)

=> s database (3a) laboratory
L9          516 DATABASE (3A) LABORATORY

=> s l9 and (cell or culture or plant)
L10         104 L9 AND (CELL OR CULTURE OR PLANT)

=> s l10 and py<2000
   1 FILES SEARCHED...
L11          26 L10 AND PY<2000

=> duplicate remove l11
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L11
L12          20 DUPLICATE REMOVE L11 (6 DUPLICATES REMOVED)

=> d 1-20 bib ab

L12  ANSWER 1 OF 20     MEDLINE on STN                    DUPLICATE 1
AN   2000077531     MEDLINE
DN   PubMed ID: 10612284
TI   The microbial proteome database--an automated laboratory
     catalogue for monitoring protein expression in bacteria.
AU   Cordwell S J; Nouwens A S; Verrills N M; McPherson J C; Hains P G; Van Dyk
     D D; Walsh B J
CS   Australian Proteome Analysis Facility, Macquarie University..
     scordwell@proteome.org.au
SO   Electrophoresis, (1999 Dec) 20 (18) 3580-8.
     Journal code: 8204476. ISSN: 0173-0835.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200001
ED   Entered STN: 20000114
     Last Updated on STN: 20000114
     Entered Medline: 20000105
AB   Laboratories devoted to high-throughput characterisation of purified
     proteins arrayed via two-dimensional (2-D) gel electrophoresis face an
     arduous task in maintaining a centralised and constantly evolving record
     of information relating to the characterisation of proteins and their
     responses following biological challenges.  The Microbial Proteome
     Database (MPD) has been conceived as an in-house resource for
     complementing the plethora of genomic databases available for such
     organisms.  The database utilises commercially available software to
     provide an electronic 'lab book' of information obtained daily from 2-D
     electrophoresis gels, image analysis packages, protein characterisation
     methodologies, and biological experimentation.  The MPD begins from a
     single 2-D gel image (a 2-D 'reference map') with clickable spots that
     link to a 'protein catalogue' (ProtCat) with spot information including
     protein identity, changes in expression determined under experimental
     conditions, cellular location, mass, and pI.  The entry for each protein
     then contains further links to gel images corresponding to the presence of
     the particular protein within different subproteomes (as defined by the pH
     of narrow- and wide-range immobilised pH gradients or from differential
     extraction methods used to determine the location of the protein within a
     functional cell).  The database currently contains information
     from strains of three microbial species (Escherichia coil, Pseudomonas
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aeruginosa and Staphylococcus aureus) and 32 master gel images. The rapid accessibility of information obtained from microbial proteomes is an essential step towards the integrated analysis of these organisms at the gene, transcript, protein and functional levels and will aid in reducing turnaround times between sample preparation and the discovery of molecules of biological significance.

L12 ANSWER 2 OF 20 MEDLINE on STN DUPLICATE 2
AN 2000080239 MEDLINE
DN PubMed ID: 10614602
TI Hospital characteristics associated with colonization of water systems by Legionella and risk of nosocomial legionnaires' disease: a cohort study of 15 hospitals.
CM Comment in: Infect Control Hosp Epidemiol. 2000 Jul;21(7):434-5. PubMed ID: 10926388
AU Kool J L; Bergmire-Sweat D; Butler J C; Brown E W; Peabody D J; Massi D S; Carpenter J C; Pruckler J M; Benson R F; Fields B S
CS Respiratory Diseases Branch, Division of Bacterial and Mycotic Diseases, Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, Georgia, USA.
SO Infection control and hospital epidemiology : official journal of the Society of Hospital Epidemiologists of America, **(1999 Dec)** 20 (12) 798-805.
Journal code: 8804099. ISSN: 0899-823X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Nursing Journals
EM 200001
ED Entered STN: 20000204
Last Updated on STN: 20010625
Entered Medline: 20000127
AB OBJECTIVE: To investigate an increase in reports of legionnaires' disease by multiple hospitals in San Antonio, Texas, and to study risk factors for nosocomial transmission of legionnaires' disease and determinants for Legionella colonization of hospital hot-water systems. SETTING: The 16 largest hospitals in the cities of San Antonio, Temple, and Austin, Texas. DESIGN: Review of **laboratory databases** to identify patients with legionnaires' disease in the 3 years prior to the investigation and to determine the number of diagnostic tests for Legionella performed; measurement of hot-water temperature and chlorine concentration and **culture** of potable water for Legionella. Exact univariate calculations, Poisson regression, and linear regression were used to determine factors associated with water-system colonization and transmission of Legionella. RESULTS: Twelve cases of nosocomial legionnaires' disease were identified; eight of these occurred in 1996. The rise in cases occurred shortly after physicians started requesting Legionella urinary antigen tests. Hospitals that frequently used Legionella urinary antigen tests tended to detect more cases of legionnaires' disease. Legionella was isolated from the water systems of 11 of 12 hospitals in San Antonio; the 12th had just experienced an outbreak of legionnaires' disease and had implemented control measures. Nosocomial legionellosis cases probably occurred in 5 hospitals. The number of nosocomial legionnaires' disease cases in each hospital correlated better with the proportion of water-system sites that tested positive for Legionella (P=.07) than with the concentration of Legionella bacteria in water samples (P=.23). Hospitals in municipalities where the water treatment **plant** used monochloramine as a residual disinfectant (n=4) and the hospital that had implemented control measures were Legionella-free. The hot-water systems of all other hospitals (n=11) were colonized with Legionella. These were all supplied with municipal drinking water that contained free chlorine as a residual disinfectant. In these contaminated hospitals, the proportion of sites testing positive was inversely correlated with free residual chlorine concentration (P=.01). In all hospitals, hot-water temperatures were too low to inhibit Legionella growth. CONCLUSIONS: The increase in reporting of nosocomial legionnaires' disease was attributable to increased use of urinary antigen tests; prior cases may have gone unrecognized. Risk of legionnaires' disease in hospital patients was better predicted by the proportion of

water-system sites testing positive for Legionella than by the measured concentration of Legionella bacteria. Use of monochloramine by municipalities for residual drinking water disinfection may help prevent legionnaires' disease.

L12 ANSWER 3 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1999:459734 BIOSIS
DN PREV199900459734
TI Software for analysis of **laboratory database** characterizing monoclonal proteins.
AU Koytcheva, N. [Reprint author]
CS Clinical Laboratory, Medical University, Sofia, Bulgaria
SO Clinical Chemistry and Laboratory Medicine, (June, 1999) Vol. 37, No. SPEC. SUPPL., pp. S248. print.
Meeting Info.: IFC-WorldLab, International Federation of Clinical and Laboratory Medicine (17th International and 13th European Congress of Clinical Chemistry and Laboratory Medicine, 1st International Congress of Clinical Molecular Biology, 31st National Congress of the Italian Society of Clinical Biochemistry and Clinical Molecular Biology). Florence, Italy. June 6-11, 1999. International Federation of Clinical and Laboratory Medicine; Italian Society of Clinical Biochemistry and Clinical Molecular Biology.
ISSN: 1434-6621.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 1 Nov 1999
Last Updated on STN: 1 Nov 1999

L12 ANSWER 4 OF 20 MEDLINE on STN
AN 1999368678 MEDLINE
DN PubMed ID: 10439805
TI CD30 expression is common in mediastinal large B-**cell** lymphoma.
CM Comment in: Am J Clin Pathol. 1999 Aug;112(2):155-8. PubMed ID: 10439794
AU Higgins J P; Warnke R A
CS Department of Pathology, Stanford University Medical Center, CA 94305, USA.
NC CA34233 (NCI)
SO American journal of clinical pathology, **(1999 Aug)** 112 (2) 241-7.
Journal code: 0370470. ISSN: 0002-9173.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199908
ED Entered STN: 19990910
Last Updated on STN: 19990910
Entered Medline: 19990824
AB Large B-**cell** lymphoma manifesting in the mediastinum shows distinctive clinical and immunophenotypic features and is recognized as a unique type of large B-**cell** lymphoma in the Revised European-American Lymphoma classification. Fifty-one cases of primary mediastinal large B-**cell** lymphoma were retrieved from the immunodiagnosis **laboratory database** files and were stained with anti-CD30 (Ber-H2). Of the 51 cases, 35 (69%) stained for CD30. This staining ranged from strong membrane staining of all or almost all of the neoplastic **cells** to positivity of rare individual **cells**. Eleven cases (22%) were negative; 4 (8%) were equivocal. Only 1 case was uninterpretable owing to B-5 fixation and lack of a positive internal control. Thus, the majority of mediastinal large B-**cell** lymphomas express the Hodgkin marker CD30. This finding may result in misdiagnosis of large **cell** lymphoma as Hodgkin disease.

L12 ANSWER 5 OF 20 MEDLINE on STN
AN 1998372682 MEDLINE

DN PubMed ID: 9708951
TI Listeriosis in pediatric oncology patients.
AU Mora J; White M; Dunkel I J
CS Department of Pediatrics, Memorial Sloan-Kettering Cancer Center, New York, New York 10021, USA.
SO Cancer, **(1998 Aug 15)** 83 (4) 817-20.
Journal code: 0374236. ISSN: 0008-543X.
CY United States
DT (CASE REPORTS)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199808
ED Entered STN: 19980910
Last Updated on STN: 19980910
Entered Medline: 19980828
AB BACKGROUND: Adult cancer patients are considered to be at an increased risk for Listeria monocytogenes infections, but, to the authors' knowledge, little information regarding this infection in the pediatric oncology population has been published. METHODS: The Memorial Sloan-Kettering Cancer Center microbiology **laboratory**'s **database** was searched for cases of Listeria monocytogenes infection during the period from January 1981 to December 1996, and thorough chart reviews of the cases identified in patients age < 21 years were performed. RESULTS: Listerial infections occurred in 5 children (3 with leukemia, 1 with lymphoma, and 1 with a brain tumor) among 20,612 admissions to the pediatric department during this period. All five children were actively receiving therapy for their malignancy, and two also were receiving other potentially immunosuppressive therapies. None was receiving co-trimoxazole prophylaxis. All were treated successfully for the Listeria monocytogenes infection with ampicillin and gentamicin (four patients) or ampicillin alone (one patient). At last follow-up two patients were long term, event-free survivors, two had died of their underlying malignancy, and one patient had died of cytomegalovirus pneumonitis. CONCLUSIONS: Listeria monocytogenes infections in pediatric oncology patients can be treated successfully with ampicillin-containing antibiotic regimens.

L12 ANSWER 6 OF 20 MEDLINE on STN DUPLICATE 3
AN 97256304 MEDLINE
DN PubMed ID: 9101635
TI Spontaneous clearance of Chlamydia trachomatis infection in untreated patients.
AU Parks K S; Dixon P B; Richey C M; Hook E W 3rd
CS Department of Medicine, University of Alabama at Birmingham 35294-0006, USA.
NC IU19 38514-9/01
SO Sexually transmitted diseases, **(1997 Apr)** 24 (4) 229-35.
Journal code: 7705941. ISSN: 0148-5717.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199706
ED Entered STN: 19970709
Last Updated on STN: 19970709
Entered Medline: 19970624
AB BACKGROUND AND OBJECTIVES: To assess the spontaneous clearance of untreated Chlamydia trachomatis infections and factors correlated with the process. STUDY DESIGN: Spontaneous clearance was assessed through review of **laboratory database**, chart review, and **laboratory** testing using direct immunofluorescence (DFA) and polymerase chain reaction (PCR) tests on C. trachomatis **culture** transport media from patients with negative chlamydial **cultures**. Specimens (C. trachomatis **culture** transport media) were obtained from patients attending a Birmingham, Alabama sexually transmitted diseases clinic. The study group consisted of patients with positive **cultures** for C. trachomatis who had repeat specimens obtained for **culture** within 45 days of initial observation and who had not

received recommended therapy for chlamydial infection in the interval between the two tests. RESULTS: Of 74 evaluable patients, 24 (32%) had negative follow-up **cultures**. **Culture** transport media for these 24 **culture**-negative patients were tested with DFA or PCR assays for chlamydial infection, and 3 (13%) were positive. **Culture** positivity rates declined significantly with increasing age and duration of follow-up. Interval treatment with benzathine penicillin resulted in apparent resolution of infection in 9 of 10 patients. Neither a history of a C. trachomatis-associated syndrome nor treatment with cefixime, metronidazole, or antifungal agents was associated with clearance of infection. CONCLUSIONS: These results are consistent with host response-mediated resolution of infection in a minority of patients and have implications regarding public health efforts to control chlamydial infection.

L12 ANSWER 7 OF 20 MEDLINE on STN
AN 97480666 MEDLINE
DN PubMed ID: 9339311
TI Health impacts of large releases of radionuclides. Impacts on **plant** and animal populations.
AU Whicker F W
CS Department of Radiological Health Sciences, Colorado State University, Fort Collins 80523, USA.
SO Ciba Foundation symposium, **(1997)** 203 74-84; discussion 84-93.
Ref: 40
Journal code: 0356636. ISSN: 0300-5208.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals; Space Life Sciences
EM 199712
ED Entered STN: 19980109
Last Updated on STN: 19990129
Entered Medline: 19971209
AB Historical experiments and observations in radioactively contaminated environments have documented radiation impacts on natural **plant** communities and animal populations. General findings from these studies are reviewed. Despite much information on the response of individual organisms to radiation in the **laboratory**, the **database** is more limited and the interpretations more complex for natural populations and communities exposed to radionuclides. These complications are discussed as they pertain to **plants** and animals in natural environments. Paradigms concerning the recovery of radiation-damaged communities and ecosystems, and areas of needed research are discussed.

L12 ANSWER 8 OF 20 MEDLINE on STN DUPLICATE 4
AN 97072109 MEDLINE
DN PubMed ID: 8914942
TI Temporal-regulation of serum lipids and stearoyl CoA desaturase and lipoprotein lipase mRNA in BALB/cHnn mice.
AU Paisley E A; Park E I; Swartz D A; Mangian H J; Visek W J; Kaput J
CS Department of Internal Medicine, University of Illinois College of Medicine, Urbana 61801, USA.
NC PHS ST32-AM07497 (OHS)
SO Journal of nutrition, **(1996 Nov)** 126 (11) 2730-7.
Journal code: 0404243. ISSN: 0022-3166.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199701
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19970113
AB Databases for genes expressed in humans or **cell cultures** are being developed as a part of the Human Genome Project. Because genomes respond to nutritional and other environmental variables,

quantitative analyses of mRNA abundance under defined nutritional and physiological states are required to understand normal metabolism and to clarify differences between normal and disease phenotypes. Reported here are comparisons of food intake, growthp5erum lipids and expression of mRNA for hepatic stearoyl CoA desaturase (Scd1) and heart lipoprotein lipase (Lpl) in female BALB/cHnn mice following food deprivation and refeeding at the end of 2 wk of feeding semipurified diets with 3, 10 or 20% corn oils. Body weights and utilization of dietary energy were similar for mice fed all three diets. There were no differences in serum lipid concentrations associated with the level of dietary fat during subsequent food deprivation and refeeding, but significant differences in serum triglycerides and total serum cholesterol were observed between food-deprived and fed mice. Heart lipoprotein lipase and hepatic Scd1 mRNA expression levels were affected significantly by concentration of corn oil and by time after eating. These and other studies examining gene regulation by dietary variables and nutrient availability are discussed in relation to development of diet-regulated gene **databases** for **laboratory** animals fed semipurified diets.

L12 ANSWER 9 OF 20 MEDLINE on STN DUPLICATE 5
AN 97029280 MEDLINE
DN PubMed ID: 8875292
TI Automatic alerts for methicillin-resistant Staphylococcus aureus surveillance and control: role of a hospital information system.
AU Pittet D; Safran E; Harbarth S; Borst F; Copin P; Rohner P; Scherrer J R; Auckenthaler R
CS Infection Control Program, University Hospital of Geneva, Switzerland.
SO Infection control and hospital epidemiology : official journal of the Society of Hospital Epidemiologists of America, **(1996 Aug)** 17 (8) 496-502.
Journal code: 8804099. ISSN: 0899-823X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Nursing Journals
EM 199701
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19970103
AB BACKGROUND: Methicillin-resistant Staphylococcus aureus (MRSA) is an escalating problem in hospitals worldwide. The hospital reservoir for MRSA includes recognized and unrecognized colonized or infected patients, as well as previously colonized or infected patients readmitted to the hospital. Early and appropriate infection control measures (ICM) are key elements to reduce MRSA transmission and to control the hospital reservoir. OBJECTIVE: To describe the role of an expert system applied to the control of MRSA at a large medical center (1,600 beds) with high endemic rates. METHODS: The University Hospital of Geneva has an extended hospital information system (HIS), DIOGENE, structured with an open distributed architecture. It includes administrative, medical, nursing, and laboratory applications with their relational databases. Among available patient **databases**, clinical microbiology **laboratory** and admission-discharge-transfer (ADT) databases are used to generate computer alerts. A laboratory alert (lab alert) is printed daily in the Infection Control Program (ICP) offices, listing all patients with **cultures** positive for MRSA detected within the preceding 24 hours. Patients might be either newly detected patients colonized or infected with MRSA, or previously recognized MRSA patients having surveillance **cultures**. The ICP nurses subsequently go to the ward or call the ward personnel to implement ICM. A second alert, the "readmission alert," detects readmission to the hospital of any patient previously colonized or infected with MRSA by periodic queries (q 1 min) to the ADT database. The readmission alert is printed in the ICP offices, but also forwarded with added guidelines to the emergency room. RESULTS: During the first 12 months of application (July 1994 to June 1995), the lab alert detected an average of 4.6 isolates per day, corresponding to 314 hospital admissions (248 patients); the use of this alert saved time for the ICP nurses by improving work organization. There were 438 readmission alerts (1.2 alerts per day) over the study period; of 347

patients screened immediately upon readmission, 114 (33%) were positive for MRSA carriage. Delayed recognition of readmitted MRSA carriers decreased significantly after the implantation of this alert; the proportion of MRSA patients recognized at the time of admission to the hospital increased from 13% in 1993 to 40% in 1995 (P < .001). CONCLUSIONS: Hospital information system-based alerts can play an important role in the surveillance and early prevention of MRSA transmission, and it can help to recognize patterns of colonization and transmission.

L12 ANSWER 10 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:394728 BIOSIS
DN PREV199699117084
TI Using WWW **databases** in investigative **laboratory** projects for **plant** physiology and molecular biology.
AU Monroe, Jonathan D. [Reprint author]; Knight, Ivor T.
CS Dep. Biol., James Madison Univ., Harrisonburg, VA 22807, USA
SO American Journal of Botany, (1996) Vol. 83, No. 6 SUPPL., pp. 216. Meeting Info.: Annual Meeting of the Botanical Society of America held with the American Institute of Biological Sciences. Seattle, Washington, USA. August 3-8, 1996.
CODEN: AJBOAA. ISSN: 0002-9122.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 3 Sep 1996
Last Updated on STN: 3 Sep 1996

L12 ANSWER 11 OF 20 MEDLINE on STN DUPLICATE 6
AN 95098062 MEDLINE
DN PubMed ID: 7528342
TI The effect of reducing the number of **cells** scored on the performance of the in vivo rat liver UDS assay.
AU Kennelly J C; Pate I; Greenwood M R
CS Zeneca Central Toxicology Laboratory, Macclesfield, Cheshire, UK.
SO Mutation research, **(1995 Feb)** 334 (1) 91-6.
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199501
ED Entered STN: 19950215
Last Updated on STN: 19960129
Entered Medline: 19950120
AB The most labour-intensive feature of the in vivo rat liver UDS assay is the scoring of hepatocyte autoradiograms by microscope. Even with image analyser and computer equipment the scoring phase of a full study might require half of the technical effort applied. Practice recommended by guidelines has been to score 50 **cells**/slide and two slides per animal. Now sufficient data have been accumulated, an evaluation was made to observe whether this procedure was necessary. An analysis of the accumulated UDS **database** in our **laboratory** was made to determine the sources of variability of mean net nuclear grain count, [N-C]. It was observed that the two largest components of variation in negative control animal mean [N-C] were between-day and interanimal variability. The contribution from sampling error during slide scoring was relatively small. Theoretical calculations showed that the greater sampling error derived from scoring 30 rather than 50 **cells** /slide would result in only a marginal increase in total assay variation. To test this, 30 **cells**/slide were randomly selected from the 50 **cells** scored originally in negative control animals in each of 18 studies over an 18-month period. It was confirmed that reducing the number of **cells** had a negligible effect on the variation of negative control animal mean [N-C] values. Furthermore, analysis of data from 10 more studies confirmed that within-study variation would be essentially unaffected by scoring 30 **cells**/slide. The use of 30 rather than 50 **cells** per slide (a total of 60 **cells**

per animal) has therefore been adopted for all current studies and scoring procedures modified to avoid operator bias during the selection of a smaller number of **cells**.

L12 ANSWER 12 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1995:34491 BIOSIS
DN PREV199598048791
TI DNA sequence from cretaceous period bone fragments.
AU Woodward, Scott R. [Reprint author]; Weyand, Nathan J.; Bunnell, Mark
CS Dep. Microbiology, 788 Widstoe Building, Brigham young Univ., Provo, UT 84602, USA
SO Science (Washington D C), (1994) Vol. 266, No. 5188, pp. 1229-1232.
CODEN: SCIEAS. ISSN: 0036-8075.
DT Article
LA English
ED Entered STN: 25 Jan 1995
Last Updated on STN: 26 Jan 1995
AB DNA was extracted from 80-million-year-old bone fragments found in strata of the Upper Cretaceous Blackhawk Formation in the roof of an underground coal mine in eastern Utah. This DNA was used as the template in a polymerase chain reaction that amplified and sequenced a portion of the gene encoding mitochondrial cytochrome b. These sequences differ from all other cytochrome b sequences investigated, including those in the GenBank and European Molecular Biology **Laboratory databases**.
DNA isolated from these bone fragments and the resulting gene sequences demonstrate that small fragments of DNA may survive in bone for millions of years.

L12 ANSWER 13 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1994:39105 BIOSIS
DN PREV199497052105
TI Evaluation of pedotransfer functions for estimating the water retention curve.
AU Tietje, Olaf [Reprint author]; Hennings, Volker
CS Sonderforschungsbereich 179, Technische Univ. Braunschweig, Langer Kamp 19c, D-38106 Braunschweig, Germany
SO Zeitschrift fuer Pflanzenernaehrung und Bodenkunde, (1993) Vol. 156, No. 5, pp. 447-455.
CODEN: ZPBOAL. ISSN: 0044-3263.
DT Article
LA German
ED Entered STN: 27 Jan 1994
Last Updated on STN: 27 Jan 1994
AB On the basis of 1693 data records of the **laboratory database** of the Lower Saxony Soil Information System (NIBIS), six pedotransfer functions for estimating the water retention curve were tested and their usefulness was evaluated. Among the three methods used to calculate water content for individual matrix potentials on the basis of linear regression analysis, the equations of Renger (1971) stand out because they yield the least deviation between the estimated and measured values. The algorithm of Vereecken et al. (1989) is the better of the two methods for estimating the parameter values of the equation of van Genuchten, describing the water retention curve by a continuous function. The methods examined here show no distinction with respect to which type of substrate that are best suited. The results allow a target-oriented selection of methods for the method database of a Soil Information System.

L12 ANSWER 14 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1993:281072 BIOSIS
DN PREV199396011297
TI Testing a method for estimating water retention parameters using the **laboratory database** of the Lower Saxony Soil Information System.
AU Hennings, Volker [Reprint author]; Mueller, Udo
CS Bundesanstalt Geowissenschaften Rohstoffe, Stilleweg 2, W-3000 Hannover 51, Germany

SO Zeitschrift fuer Pflanzenernaehrung und Bodenkunde, (1993) Vol. 156, No. 1, pp. 67-73.
CODEN: ZPBOAL. ISSN: 0044-3263.
DT Article
LA German
ED Entered STN: 9 Jun 1993
Last Updated on STN: 9 Jun 1993
AB The validity of the method used for estimating field capacity (pF gt 1.8), **plant** available water (pF 1.8-4.2), air capacity (pF lt 1.8), and total pore volume from soil texture, packing density (bulk density + 0.009% clay) and human content described by the Arbeitsgruppe Bodenkunde (1982) was checked on the basis of 1693 pF curves of the **laboratory database** of the Lower Saxony Soil Information System (NIBIS). The positive and negative corrections for humus content applied in this method to the above parameters are clearly too small. Use of tables for estimating the pore volume of humus-free soils leads to overestimation. It will only be possible to work out an alternative method applicable to all classes of soils when the database has been extended.

L12 ANSWER 15 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1993:249654 BIOSIS
DN PREV199395128829
TI Mouse liver protein database: A catalog of proteins detected by two-dimensional gel electrophoresis.
AU Giometti, Carol S. [Reprint author]; Taylor, John; Tollaksen, Sandra L.
CS Argonne Natl. Lab., Build. 202, Room B 117, 9700 S. Cass Ave., Argonne, IL 60439, USA
SO Electrophoresis, (1992) Vol. 13, No. 12, pp. 970-991.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 21 May 1993
Last Updated on STN: 21 May 1993
AB Alterations in the abundance or structure of mouse liver proteins are being studied using two-dimensional gel electrophoresis (2-DE) to build a database of protein changes correlating with exposure to ionizing radiation or toxic chemicals. Thus far, studied have included the analysis of proteins from the offspring of exposed parents or from the exposed individuals themselves. In order to characterize and identify proteins found altered by such exposures, sex- and strain-related differences in protein patterns have been analyzed, and the subcellular locations of a large portion of the mapped proteins have been determined. As part of these studies, data are collected and stored using a variety of computer hardware and software tools that allow the accumulation of information on the origin of samples, gel identification, experiment description, and protein similarities and differences. This accumulation of information constitutes the mouse liver protein database. Relational database software is used to tie the different facets of the databae together so that the results of a variety of experiments can be compared and interrelated. The database optimizes the information obtained from 2-DE gel sets by allowing use of the data for many purposes, including monitoring of gel resolution to ensure the collection of high quality data and correlation of protein effects induced by different agents. This first edition of the Argonne National **Laboratory** mouse liver protein **database** lays the foundation for future work and communication that should elucidate the significance of observed protein effects as possible markers of exposure to toxic agents.

L12 ANSWER 16 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1992:163534 BIOSIS
DN PREV199293085859; BA93:85859
TI INTEGRATION OF A BARCODE READER WITH A COMMERCIAL FLOW CYTOMETER.
AU ROBINSON J P [Reprint author]; MAGUIRE D; KING G; KELLEY S; DURACK G
CS PURDUE UNIV CYTOMETRY LAB, HANSEN LIFE SCI RES BLDG, B050, WEST LAFAYETTE, INDIANA 47907, USA
SO Cytometry, (1992) Vol. 13, No. 2, pp. 193-197.

CODEN: CYTODQ. ISSN: 0196-4763.
DT Article
Software Review
FS BA
LA ENGLISH
ED Entered STN: 31 Mar 1992
Last Updated on STN: 31 Mar 1992
AB This report describes the application and installation of a barcode reader on a standard EPICS Elite flow cytometer. The barcode reader system eliminates keyboard entry of sample information on the cytometer. The system automates the transfer of sample information already present in our **laboratory database** to the cytometer at run time. The system uses a standard "off-the-shelf" bar code wand with a personal computer keyboard interface and requires no additional software at run time. No typing of sample information is required by the operator at any stage of normal sample operation at the cytometer. All operations are automatically coded into the cytometry software using the macro functions of the software. Tubes are inserted into the tube reader and sample information is transferred automatically into the cytometer. We have found that the system allows rapid and continuous operation of routine clinical and research samples. This automated data entry also reduces the possibility of data input errors.

L12 ANSWER 17 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1990:383078 BIOSIS
DN PREV199090069759; BA90:69759
TI MEASUREMENT OF HUMAN CHORIONIC GONADOTROPIN DURING EARLY PREGNANCY A COMPARISON OF TWO IMMUNORADIOMETRIC ASSAYS.
AU MATSON P L [Reprint author]; NEWMAN M C; MORROLL D; TROUP S A; LIEBERMAN B A
CS REGIONAL IVF UNIT, ST MARY'S HOSPITAL, WHITWORTH PARK, MANCHESTER M13 0JH, UK
SO Journal of In Vitro Fertilization and Embryo Transfer, (1990) Vol. 7, No. 3, pp. 168-171.
ISSN: 0740-7769.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 21 Aug 1990
Last Updated on STN: 22 Aug 1990
AB Evidence of implantation following either in vitro fertilization and embryo transfer (IVF-ET) or gamete intrafallopian transfer (GIFT) was obtained by collecting blood on days 10, 12, 14, 16, and 18 after oocyte recovery (day 0), and retrospectively measuring human chorionic gonadotropin (hCG). This was done using immunoradiometric assays for hCG, manufactured either by Serono Diagnostics Ltd. (MAIAclone) or Diagnostics Products Corporation (IRMA-count). The analysis of 63 serum samples by both kits showed a good correlation ($r = 0.99$) but the Serono (y) method gave values which were consistently greater ($y = 1.58x + 4.89$) than those of the DPC (x) method. A comparison of the hCG profile of singleton pregnancies measured with either the Serono ($n = 33$) or DPC ($n = 22$) kits gave a similar relationship. These results suggest that great care must be taken when comparing results from different laboratories using different kits. Also, consideration must be given to the possible loss of a continuous **database** should a **laboratory** change kit.

L12 ANSWER 18 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1990:174833 BIOSIS
DN PREV199089092003; BA89:92003
TI GEOGRAPHIC ORIGIN ON RED-WINGED BLACKBIRDS RELATIVE TO RICE **CULTURE** IN SOUTHWESTERN AND SOUTHCENTRAL LOUISIANA USA.
AU BRUGGER K E [Reprint author]; DOLBEER R A
CS US DEP AGRIC, DENVER WILDLIFE RES CENT, 2820 EAST UNIVERSITY AVE, GAINESVILLE, FLA 32601, USA
SO Journal of Field Ornithology, (1990) Vol. 61, No. 1, pp. 90-97.
ISSN: 0273-8570.
DT Article

FS BA
LA ENGLISH
ED Entered STN: 10 Apr 1990
Last Updated on STN: 10 Apr 1990
AB The 62-year (1924-1985) U.S. Fish and Wildlife Service Bird Banding Laboratory recovery-retrieval file for 12,020 Red-winged Blackbirds (Agelaius phoeniceus) was summarized to identify the geographic origin of birds in southwestern and southcentral Louisiana in relation to the rice-growing cycle. Of 58 recoveries not at banding stations, 38 (66%) were in winter and 13 of these (34%) were local Louisiana birds. Resident birds constituted 16 of 20 nonbanding station recoveries from spring planting season to autumn second harvest. Analyses that included recoveries made at banding stations yielded substantial increases in number of resident birds present during planting and second harvest, suggesting that local birds are responsible for most crop damage by redwings during those phases of rice **culture**. However, a bias toward resident redwings was evident in the banding station recoveries. Efforts to band or mass-mark Red-winged Blackbirds in winter should be increased substantially to provide an expanded data base for evaluating the relationship of migration and rice damage in the gulf coastal region.

L12 ANSWER 19 OF 20 MEDLINE on STN
AN 90121781 MEDLINE
DN PubMed ID: 2692617
TI Risk assessment of the mycotoxin ochratoxin A.
AU Kuiper-Goodman T; Scott P M
CS Bureau of Chemical Safety, Health and Welfare Canada, Ottawa, Ontario.
SO Biomedical and environmental sciences : BES, **(1989 Sep)** 2 (3) 179-248. Ref: 378
Journal code: 8909524. ISSN: 0895-3988.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199003
ED Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19900306
AB Ochratoxin A (OA) is a mycotoxin which has been found to occur in foods of **plant** origin, in edible animal tissues, as well as in human blood sera and tissues. The ability of OA to move up the food chain is aided by its long half-life in certain edible animal species. In this report, an evaluation of the health risks to Canadians due to the presence of OA in food products is presented. The first part of the report deals with the physicochemical aspects, mycology, laboratory production, analytical methods, and natural occurrence in **plant** products, animal products, and human tissues. The stability of OA in foods and feeds, the effects of food processing, and the removal from foods and feeds by physiochemical means are also discussed. From these data, the worst case estimate for the daily exposure of Canadians to OA, from the consumption of pork-based food products and cereal foods, is approximately 5 ng OA/kg body wt (mean of eaters) for young children, the highest consumption group on a body weight basis. The second part of the report deals with the metabolic disposition as well as the available toxicity **database** for OA in **laboratory** animals, farm animals, and humans. The major target for OA toxicity in all mammalian species tested is the kidney, and endemic nephropathies affecting livestock as well as humans have been attributed to OA. OA is also teratogenic, and in the fetus the major target is the developing central nervous system. Recent studies have provided "clear evidence" of the carcinogenicity of OA in two rodent species. OA was found to be nonmutagenic in various microbial and mammalian gene mutation assays, but weak genotoxic activity to mammalian **cells** was noted. In addition, OA was found to suppress immune function. Based on the NTP carcinogenicity study with OA in rats, the estimated tolerable daily intake in humans ranges from 0.2 to 4.2 ng OA/kg body wt, depending on the method of extrapolation used. In view of the toxic properties of OA, it is recommended that exposure to OA be kept to a

minimum. In Canada, further monitoring programs are required to better define the overall residue profile of OA in cereal grains, animal feeds, animal food products, and human blood. Such data are required to better assess dietary exposure and to ascertain the need for regulatory controls or other control mechanisms.

L12 ANSWER 20 OF 20 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1987:392779 BIOSIS
DN PREV198733072919; BR33:72919
TI COMPUTER INTENSIVE ENHANCEMENTS TO THE CLINICAL **LABORATORY** IMAGE CYTOMETRY AND **DATABASE** DERIVED DECISION TABLES.
AU GOIN J E [Reprint author]
CS ANALYTICAL DATA SYSTEMS, RADNOR, PENNSYLVANIA, USA
SO Clinical Chemistry, (1987) Vol. 33, No. 6, pp. 868.
Meeting Info.: 39TH NATIONAL MEETING OF THE AMERICAN ASSOCIATION FOR CLINICAL CHEMISTRY, SAN FRANCISCO, CALIFORNIA, USA, JULY 19-24, 1987. CLIN CHEM.
CODEN: CLCHAU. ISSN: 0009-9147.
DT Conference; (Meeting)
FS BR
LA ENGLISH
ED Entered STN: 12 Sep 1987
Last Updated on STN: 12 Sep 1987

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☐	L2	2000	19
☐	L1	laboratory information management system	168

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                    STN Express with Discover!
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 NEWS 12  SEP 14    STN Patent Forum to be held October 13, 2004, in Iselin, NJ
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 NEWS 14  SEP 27    SWETSCAN will no longer be available on STN

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               AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004
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L1             2 (LIMS OR LABORATORY INFORMATION MANAGEMENT SYSTEM) AND CELL

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L1 ANSWER 1 OF 2 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:478495 BIOSIS
DN PREV199699208051
TI Loss of extremities in cases of heparin-induced thrombocytopenia.
AU Wenzl, M. E. [Reprint author]; Leffringhausen, W.; Scherlitzky, L.
CS Berufsgenossenschaftliches Unfallkrankenhaus, Bergedorfer Str. 10, D-21033 Hamburg, Germany
SO Unfallchirurg, (1996) Vol. 99, No. 8, pp. 607-611.
ISSN: 0177-5537.
DT Article
LA German
ED Entered STN: 24 Oct 1996
Last Updated on STN: 24 Oct 1996
AB We report the cases of two patients who last ***lims*** as a result of heparin-induced thrombocytopenia (HIT). On the basis of these cases, the incidence, pathophysiology and the diagnosis of HIT are reviewed. For the diagnosis of HIT, the platelet aggregation test and ELISA are used. For HIT prophylaxis and treatment thromboembolic complications is recommended Orgaran. Exact dosage schedules are provided.

L1 ANSWER 2 OF 2 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1990:112016 BIOSIS
DN PREV199089061507; BA89:61507
TI NEUROPATHOLOGY OF GRACILE AXONAL DYSTROPHY GAD MOUSE AN ANIMAL MODEL OF CENTRAL DISTAL AXONOPATHY IN PRIMARY SENSORY NEURONS.
AU MUKOYAMA M [Reprint author]; YAMAZAKI K; KIKUCHI T; TOMITA T
CS CHUBU NATL HOSP, 36-3 GENGO, MORIOKA, OHBU, AICHI 474, JPN
SO Acta Neuropathologica, (1989) Vol. 79, No. 3, pp. 294-299.
CODEN: ANPTAL. ISSN: 0001-6322.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 21 Feb 1990
Last Updated on STN: 21 Feb 1990
AB A new neurological mutant mouse shows a gracile axonal dystrophy (GAD). The degenerative lesion develops by postnatal day 80, first appearing in the most rostral portion of the gracile fascicles. This lesion then extends caudally to involve the entire gracile fascicles. Many axonal swellings (dystrophies) also appear in the degenerative lesions in proportion to their severity. The clinical findings develop in keeping with these pathological changes, and are characterized by tremor, ataxia and difficulty in moving the hid ***lims*** . These start around day 80, and progress gradually to death about day 150. The lumbar dorsal roots, their spinal root ganglia and peripheral nerves are normal. Electron microscopic study shows dystrophic axons packed with neurofilaments, mitochondria and tubulovesicular structures. These may reflect some stagnation of axonal transport. The distribution of the lesions suggest that the GAD mouse has a central distal axonopathy involving primary sensory neurons of the lumbar dorsal root ganglia.

=> s laboratory information management system
L2 86 LABORATORY INFORMATION MANAGEMENT SYSTEM

=> s l2 and review/dt
L3 2 L2 AND REVIEW/DT

=> d 1-2 bib ab

L3 ANSWER 1 OF 2 MEDLINE on STN
AN 2002634193 MEDLINE
DN PubMed ID: 12393930
TI From information management to protein annotation: preparing protein structures for drug discovery.
AU Peat Tom; de La Fortelle Eric; Culpepper Janice; Newman Janet
CS Structural GenomiX Inc, USA.
SO Acta crystallographica. Section D, Biological crystallography, (2002 Nov) 58 (Pt 11) 1968-70. Ref: 2
Journal code: 9305878. ISSN: 0907-4449.
CY Denmark
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals

EM 200305
ED Entered STN: 20021024
Last Updated on STN: 20030508
Entered Medline: 20030507
AB In contrast to academic pursuits of structural genomics, Structural GenomiX (SGX) solves protein structures at high throughput for the main purpose of enhancing drug-discovery projects, either internally or in partnership with pharmaceutical/biotechnology companies. This involves a radical redesign of the pipeline of methods that turn a gene sequence into a three-dimensional protein structure. The various processes all report electronically to a ***Laboratory*** ***Information*** ***Management*** ***System*** (LIMS) to make sure all the parameters of the experiment are recorded in an accessible and 'mineable' form, helping guarantee reproducibility of results. Quality control at several key points keeps the process from branching out on a wrong hypothesis. Protein annotation, in a broad sense, takes care of the interpretation of a protein crystal structure or the crystal structure of one or several protein-ligand complexes. This interpretation both gathers all necessary biological information (protein function, mechanism, specific features within a protein family etc.) and hands over this information in a form accessible to medicinal chemistry teams designing specific small-molecule agonists or antagonists.

L3 ANSWER 2 OF 2 MEDLINE on STN
AN 89359742 MEDLINE
DN PubMed ID: 2671006
TI Robotics in biomedical chromatography and electrophoresis.
AU Fouda H G
CS Drug Metabolism Department, Central Research, Pfizer Inc., Groton, CT 06340.
SO Journal of chromatography, (1989 Aug 11) 492 85-108. Ref: 90
Journal code: 0427043. ISSN: 0021-9673.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 198910
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19891010
AB The ideal laboratory robot can be viewed as "an indefatigable assistant capable of working continuously for 24 h a day with constant efficiency". The development of a system approaching that promise requires considerable skill and time commitment, a thorough understanding of the capabilities and limitations of the robot and its specialized modules and an intimate knowledge of the functions to be automated. The robot need not emulate every manual step. Effective substitutes for difficult steps must be devised. The future of laboratory robots depends not only on technological advances in other fields, but also on the skill and creativity of chromatographers and other scientists. The robot has been applied to automate numerous biomedical chromatography and electrophoresis methods. The quality of its data can approach, and in some cases exceed, that of manual methods. Maintaining high data quality during continuous operation requires frequent maintenance and validation. Well designed robotic systems can yield substantial increase in the laboratory productivity without a corresponding increase in manpower. They can free skilled personnel from mundane tasks and can enhance the safety of the laboratory environment. The integration of robotics, chromatography systems and ***laboratory*** ***information*** ***management*** ***systems*** permits full automation and affords opportunities for unattended method development and for future incorporation of artificial intelligence techniques and the evolution of expert systems. Finally, humanoid attributes aside, robotic utilization in the laboratory should not be an end in itself. The robot is a useful tool that should be utilized only when it is prudent and cost-effective to do so.

=> d his

(FILE 'HOME' ENTERED AT 13:23:34 ON 29 SEP 2004)

FILE 'MEDLINE, BIOSIS' ENTERED AT 13:31:39 ON 29 SEP 2004
L1 2 S (LIMS OR LABORATORY INFORMATION MANAGEMENT SYSTEM) AND CELL

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L2            86 S LABORATORY INFORMATION MANAGEMENT SYSTEM
L3             2 S L2 AND REVIEW/DT

=> s l2 and (plant or cell or culture)
L4             9 L2 AND (PLANT OR CELL OR CULTURE)

=> duplicate remove l4
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L4
L5             8 DUPLICATE REMOVE L4  (1 DUPLICATE REMOVED)

=> d 1-8 bib ab

L5   ANSWER 1 OF 8     MEDLINE on STN                        DUPLICATE 1
AN   2003516612     MEDLINE
DN   PubMed ID: 14594706
TI   Development of an integrated   ***laboratory***     ***information***
       ***management***     ***system***   for the maize mapping project.
AU   Sanchez-Villeda H; Schroeder S; Polacco M; McMullen M; Havermann S; Davis
     G; Vroh-Bi I; Cone K; Sharopova N; Yim Y; Schultz L; Duru N; Musket T;
     Houchins K; Fang Z; Gardiner J; Coe E
CS   Department of Agronomy, Division of Biological Sciences and USDA-ARS,
     University of Missouri, Columbia, MO 65211, USA.
SO   Bioinformatics (Oxford, England), (2003 Nov 1) 19 (16) 2022-30.
     Journal code: 9808944. ISSN: 1367-4803.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200404
ED   Entered STN: 20031104
     Last Updated on STN: 20040414
     Entered Medline: 20040413
AB   MOTIVATION: The development of an integrated genetic and physical map for
     the maize genome involves the generation of an enormous amount of data.
     Managing this data requires a system to aid in genotype scoring for
     different types of markers coming from both local and remote users.  In
     addition, researchers need an efficient way to interact with genetic
     mapping software and with data files from automated DNA sequencing.  They
     also need ways to manage primer data for mapping and sequencing and
     provide views of the integrated physical and genetic map and views of
     genetic map comparisons.  RESULTS: The MMP-LIMS system has been used
     successfully in a high-throughput mapping environment.  The genotypes from
     957 SSR, 1023 RFLP, 189 SNP, and 177 InDel markers have been entered and
     verified via MMP-LIMS.  The system is flexible, and can be easily modified
     to manage data for other species.  The software is freely available.
     AVAILABILITY: To receive a copy of the iMap or cMap software, please fill
     out the form on our website.  The other MMP-LIMS software is freely
     available at http://www.maizemap.org/bioinformatics.htm.

L5   ANSWER 2 OF 8  BIOSIS  COPYRIGHT (c) 2004 The Thomson Corporation.  on STN
AN   2003:417167  BIOSIS
DN   PREV200300417167
TI   Yeast structural genomics: High throughput production and crystallization
     of large sets of eukaryotic proteins.
AU   van Tilbeurgh, H. [Reprint Author]
CS   CNRS-UMR9920, Gif sur Yvette, France
SO   European Biophysics Journal, (June 2003) Vol. 32, No. 3, pp. 173. print.
     Meeting Info.: 4th European Biophysics Congress. Alicante, Spain. July
     05-09, 2003. European Biophysical Societies' Association (EBSA); Spanish
     Biophysics Society.
     CODEN: EBJOE8. ISSN: 0175-7571.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 10 Sep 2003
     Last Updated on STN: 10 Sep 2003

L5   ANSWER 3 OF 8  BIOSIS  COPYRIGHT (c) 2004 The Thomson Corporation.  on STN
AN   2002:587627  BIOSIS
DN   PREV200200587627
TI   Gene expression profiling in an era of high-throughput biology.
AU   Hurban, Patrick [Reprint author]
CS   Paradigm Genetics, Inc., Research Triangle Park, NC, USA
```

phurban@paradigmgenetics.com
SO Plant Biology (Rockville), (2002) Vol. 2002, pp. 6. print.
Meeting Info.: Annual Meeting of the American Society of Plant Biologists on Plant Biology. Denver, CO, USA. August 03-07, 2002. American Society of Plant Biologists.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 13 Nov 2002
Last Updated on STN: 13 Nov 2002

L5 ANSWER 4 OF 8 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2000:486729 BIOSIS
DN PREV200000486729
TI A ***laboratory*** ***information*** ***management*** ***system*** for small to medium sized soil, ***plant*** and water testing laboratories.
AU Luciuk, Rodney [Reprint author]; Winkleman, Gary E. [Reprint author]; Sluser, Mark [Reprint author]; Taylor, Patrick A. [Reprint author]; Ens, Arnie M. [Reprint author]
CS Semiarid Prairie Agricultural Research Centre, Agricultural and Agri-Food Canada, Swift Current, SK, S9H 3X2, Canada
SO Communications in Soil Science and Plant Analysis, (June/July, 2000) Vol. 31, No. 11-14, pp. 1965-1972. print.
Meeting Info.: 1999 International Symposium on Soil and Plant Analysis. Brisbane, Queensland, Australia. March 22-26, 1999.
CODEN: CSOSA2. ISSN: 0010-3624.
DT Conference; (Meeting)
Conference; (Meeting Poster)
Conference; (Meeting Paper)
LA English
ED Entered STN: 8 Nov 2000
Last Updated on STN: 10 Jan 2002

L5 ANSWER 5 OF 8 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2000:480930 BIOSIS
DN PREV200000480930
TI A ***laboratory*** ***information*** ***management*** ***system*** for small to medium sized soil, ***plant*** and water testing laboratories.
AU Luciuk, R. [Reprint author]; Taylor, P. A. [Reprint author]; Winkleman, G. E. [Reprint author]
CS Semiarid Prairie Agricultural Research Centre, (SPARC), Agriculture and Agri-Food Canada, Swift Current, SK, S9H 3X2, Canada
SO Communications in Soil Science and Plant Analysis, (June/July, 2000) Vol. 31, No. 11-14, pp. 1400. print.
Meeting Info.: 1999 International Symposium on Soil and Plant Analysis. Brisbane, Queensland, Australia. March 22-26, 1999.
CODEN: CSOSA2. ISSN: 0010-3624.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 8 Nov 2000
Last Updated on STN: 10 Jan 2002

L5 ANSWER 6 OF 8 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:213295 BIOSIS
DN PREV199698769424
TI Soilims: A low-budget, user-friendly ***laboratory*** ***information*** ***management*** ***system*** for small to medium-sized soil, ***plant*** , and water laboratories.
AU Brunt, J.; Van Reeuwijk, L. P.
CS International Soil Reference Information Cent., P.O. Box 353, 6700 AJ Wageningen, Netherlands
SO Communications in Soil Science and Plant Analysis, (1996) Vol. 27, No. 3-4, pp. 201-202.
Meeting Info.: International Symposium on Soil Testing and Plant Analysis: Quality of Soil and Plant Analysis in View of Sustainable Agriculture and the Environment, Part I. Wageningen, Netherlands. August 5-10, 1995.
CODEN: CSOSA2. ISSN: 0010-3624.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 2 May 1996
Last Updated on STN: 2 May 1996

L5 ANSWER 7 OF 8 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:192773 BIOSIS
DN PREV199698748902
TI High throughput screening for new drug discovery.
AU Lin, Bing Bing
CS Panlabs Taiwan Ltd., 158 Li-Teh Rd., Pei-Tou, Taipei 112, Taiwan
SO Journal of Food and Drug Analysis, (1995) Vol. 3, No. 4, pp. 233-241.
ISSN: 1021-9498.
DT Article
LA English
ED Entered STN: 2 May 1996
Last Updated on STN: 2 May 1996
AB The world pharmaceutical market, which was valued at 247.9 billion in 1994, is forecasted to grow to 342 billion by 1999. High throughput screening(HTS) is attracting attention as a novel methodology for new drug discovery. HTS is expected to expand the scale from one thousand to one hundred thousand times the current level by utilizing robots, ***laboratory*** ***information*** ***management*** ***systems*** (LIMS), various sources to screen natural products(***plant*** extracts, secondary microbial metabolites), peptide combinatorial libraries and combinatorial organic synthesis(COS) for new therapeutics. Instrumentation, target selection, source material, sample preparation, primary and secondary assays, isolation, purification and structure elucidation are all important for HTS.

L5 ANSWER 8 OF 8 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1991:33976 BIOSIS
DN PREV199140010956; BR40:10956
TI COMPUTERIZATION OF MYCOLOGICAL COLLECTION DATA OF THE AMERICAN TYPE ***CULTURE*** COLLECTION.
AU JONG S C [Reprint author]; BIRMINGHAM J M; KUHAYDA P S; HATT H D; EDWARDS M J
CS AMERICAN TYPE CULTURE COLLECTION, 12301 PARKLAWN DRIVE, ROCKVILLE, MD 20852, USA
SO Sydowia, (1990) Vol. 42, pp. 231-245.
CODEN: SYAMAU. ISSN: 0082-0598.
DT Article
FS BR
LA ENGLISH
ED Entered STN: 5 Jan 1991
Last Updated on STN: 5 Jan 1991

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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	42.97	45.91

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                    resulting in a closer connection to BABS
 NEWS  4  AUG 02    IFIPAT/IFIUDB/IFICDB reloaded with new search and display
                    fields
 NEWS  5  AUG 02    CAplus and CA patent records enhanced with European and Japan
                    Patent Office Classifications
 NEWS  6  AUG 02    The Analysis Edition of STN Express with Discover!
                    (Version 7.01 for Windows) now available
 NEWS  7  AUG 27    BIOCOMMERCE: Changes and enhancements to content coverage
 NEWS  8  AUG 27    BIOTECHABS/BIOTECHDS: Two new display fields added for legal
                    status data from INPADOC
 NEWS  9  SEP 01    INPADOC: New family current-awareness alert (SDI) available
 NEWS 10  SEP 01    New pricing for the Save Answers for SciFinder Wizard within
                    STN Express with Discover!
 NEWS 11  SEP 01    New display format, HITSTR, available in WPIDS/WPINDEX/WPIX
 NEWS 12  SEP 14    STN Patent Forum to be held October 13, 2004, in Iselin, NJ
 NEWS 13  SEP 27    STANDARDS will no longer be available on STN
 NEWS 14  SEP 27    SWETSCAN will no longer be available on STN

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               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004
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FILE 'HOME' ENTERED AT 14:24:45 ON 29 SEP 2004

=> s high throughput screening and laboratory information management system
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files.  For example, the EXPAND
command can only be used to look at the index in a file which has an
index.  Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of
commands which can be used in this file.

=> file .pub
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                      ENTRY     SESSION
FULL ESTIMATED COST                                    1.26        1.26

FILE 'MEDLINE' ENTERED AT 14:28:14 ON 29 SEP 2004

FILE 'BIOSIS' ENTERED AT 14:28:14 ON 29 SEP 2004
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=> s high throughput screening and laboratory information management system
L1             1 HIGH THROUGHPUT SCREENING AND LABORATORY INFORMATION MANAGEMENT
                 SYSTEM

=> d bib ab

L1   ANSWER 1 OF 1  BIOSIS  COPYRIGHT (c) 2004 The Thomson Corporation.  on STN
AN   1996:192773  BIOSIS
DN   PREV199698748902
TI     ***High***     ***throughput***     ***screening***   for new drug
     discovery.
AU   Lin, Bing Bing
CS   Panlabs Taiwan Ltd., 158 Li-Teh Rd., Pei-Tou, Taipei 112, Taiwan
SO   Journal of Food and Drug Analysis, (1995) Vol. 3, No. 4, pp. 233-241.
     ISSN: 1021-9498.
DT   Article
LA   English
ED   Entered STN: 2 May 1996
     Last Updated on STN: 2 May 1996
AB   The world pharmaceutical market, which was valued at 247.9 billion in
     1994, is forecasted to grow to 342 billion by 1999.    ***High***
       ***throughput***     ***screening***  (HTS) is attracting attention as a
     novel methodology for new drug discovery.  HTS is expected to expand the
     scale from one thousand to one hundred thousand times the current level by
     utilizing robots,   ***laboratory***     ***information***
       ***management***     ***systems***  (LIMS), various sources to screen
     natural products(plant extracts, secondary microbial metabolites), peptide
     combinatorial libraries and combinatorial organic synthesis(COS) for new
     therapeutics.  Instrumentation, target selection, source material, sample
     preparation, primary and secondary assays, isolation, purification and
     structure elucidation are all important for HTS.


=> s laboratory information management system
L2           86 LABORATORY INFORMATION MANAGEMENT SYSTEM

=> duplicate remove l2
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L2
L3            74 DUPLICATE REMOVE L2 (12 DUPLICATES REMOVED)

=> d 1-10 bib ab

L3   ANSWER 1 OF 74     MEDLINE on STN
AN   2004371299     IN-PROCESS
DN   PubMed ID: 15274127
TI   In vitro and in silico processes to identify differentially expressed
     proteins.
AU   Allet Nadia; Barrillat Nicolas; Baussant Thierry; Boiteau Celia; Botti
     Paolo; Bougueleret Lydie; Budin Nicolas; Canet Denis; Carraud Stephanie;
     Chiappe Diego; Christmann Nicolas; Colinge Jacques; Cusin Isabelle;
     Dafflon Nicolas; Depresle Benoit; Fasso Irene; Frauchiger Pascal; Gaertner
     Hubert; Gleizes Anne; Gonzalez-Couto Eduardo; Jeandenans Catherine;
     Karmime Abderrahim; Kowall Thomas; Lagache Sophie; Mahe Eve; Masselot
     Alexandre; Mattou Hassan; Moniatte Marc; Niknejad Anne; Paolini Marianne;
     Perret Frederic; Pinaud Nicolas; Ranno Frederic; Raimondi Sylvain; Reffas
     Samia; Regamey Pierre-Olivier; Rey Pierre-Antoine; Rodriguez-Tome
     Patricia; Rose Keith; Rossellat Gerald; Saudrais Cedric; Schmidt Camille;
     Villain Matteo; Zwahlen Catherine
CS   GeneProt Inc., Meyrin, Switzerland.
SO   Proteomics, (2004 Aug) 4 (8) 2333-51.
     Journal code: 101092707. ISSN: 1615-9853.
CY   Germany: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   IN-PROCESS; NONINDEXED; Priority Journals
ED   Entered STN: 20040728
     Last Updated on STN: 20040818
AB   We present an integrated proteomics platform designed for performing
     differential analyses.  Since reproducible results are essential for
     comparative studies, we explain how we improved reproducibility at every
     step of our laboratory processes, e.g. by taking advantage of the powerful
```

laboratory ***information*** ***management***
system we developed. The differential capacity of our platform is validated by detecting known markers in a real sample and by a spiking experiment. We introduce an innovative two-dimensional (2-D) plot for displaying identification results combined with chromatographic data. This 2-D plot is very convenient for detecting differential proteins. We also adapt standard multivariate statistical techniques to show that peptide identification scores can be used for reliable and sensitive differential studies. The interest of the protein separation approach we generally apply is justified by numerous statistics, complemented by a comparison with a simple shotgun analysis performed on a small volume sample. By introducing an automatic integration step after mass spectrometry data identification, we are able to search numerous databases systematically, including the human genome and expressed sequence tags. Finally, we explain how rigorous data processing can be combined with the work of human experts to set high quality standards, and hence obtain reliable (false positive < 0.35%) and nonredundant protein identifications.

L3 ANSWER 2 OF 74 MEDLINE on STN
AN 2004453597 IN-PROCESS
DN PubMed ID: 15360612
TI A unified ***laboratory*** ***information*** ***management*** ***system*** for research data.
AU Ochs M F; Goralczyk E M; Grant J D; Manion F J; Yeung A; Seeholzer S; Mathew G; Hardy R R; Beck J R
SO Medinfo, (2004) 2004 (CD) 1784.
Journal code: 7600347. ISSN: 1569-6332.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040914
Last Updated on STN: 20040914
AB High throughput technologies, such as microarrays, array cytogenetic hybridization (CGH), proteomics, immuno-fluorescence imaging, and flow cytometry, are revolutionizing biomedical research. These technologies lead to large data sets, ranging from hundreds of gigabytes to terabytes per year, including raw image and quantified data as well as processed data. As these data provide insights into the fundamental cellular behaviors of normal and diseased tissues, their potential for application in therapy is enormous. However, to realize this potential, the data must be gathered with good quality control, with maintenance of protocol details, and in a manner that allows integration with clinical, drug treatment, outcomes, and other data. Presently, each field has adopted different data storage standards, sometimes with a dedicated ***laboratory*** ***information*** ***management*** ***system*** (LIMS) and sometimes with simple file storage. We present here a different approach, aimed at developing technology-specific LIMS implementations within a single system.

L3 ANSWER 3 OF 74 MEDLINE on STN
AN 2004427607 IN-PROCESS
DN PubMed ID: 15333956
TI CLIMS: Crystallography ***Laboratory*** ***Information*** ***Management*** ***System***
AU Fulton Kate F; Ervine Shaun; Faux Noel; Forster Richard; Jodun Rachel A; Ly Wayson; Robilliard Lee; Sonsini Jai; Whelan Dan; Whisstock James C; Buckle Ashley M
CS The Department of Biochemistry and Molecular Biology, School of Biomedical Sciences, Faculty of Medicine, Monash University, Clayton, Victoria 3800, Australia.
SO Acta crystallographica. Section D, Biological crystallography, (2004 Sep) 60 (Pt 9) 1691-3.
Journal code: 9305878. ISSN: 0907-4449.
CY Denmark
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040831
Last Updated on STN: 20040831
AB Macromolecular crystallography requires simple yet effective means of organizing and managing the large amounts of data generated by crystallization experiments. There are several freely available web-based ***Laboratory*** ***Information*** ***Management***

Systems (LIMS) that assist in these tasks. These, however, rely on the limited user interfaces allowed in HTML-based web pages. To address this limitation, a new LIMS for protein crystallization, which features a novel rich graphical user interface (GUI) to a relational database, has been developed. This application, which is called CLIMS (Crystallography LIMS), assists in all aspects of protein-crystallization projects: protein expression, handling, crystallization optimization, visualization of results and preliminary diffraction data. Extensive use of templates, particularly for commercial screens and common optimization grid screens, exploits the redundancy in experimental setups. The crystallization tray is the central focus of the graphical interface, thus facilitating rapid visualization and annotation of results. CLIMS was developed specifically to cater for the needs of individual laboratories requiring an intuitive and robust system for managing crystallization experiments and is freely available.

L3 ANSWER 4 OF 74 MEDLINE on STN
AN 2004477296 IN-PROCESS
DN PubMed ID: 15389322
TI LIMaS: the JAVA-based application and database for microarray experiment tracking.
AU Webb Sarah C; Attwood Anthony; Brooks Tony; Freeman Tom; Gardner Phil; Pritchard Clare; Williams Debbie; Underhill Peter; Strivens Mark A; Greenfield Andy; Pilicheva Ekaterina
CS CEH-Oxford, Mansfield Road, OX1 3SR, Oxford, Oxfordshire, UK,. scwe@ceh.ac.uk
SO Mammalian genome : official journal of the International Mammalian Genome Society, (2004 Sep) 15 (9) 740-7.
Journal code: 9100916. ISSN: 0938-8990.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20040925
Last Updated on STN: 20040925
AB Microarrays allow monitoring of gene expression for tens of thousands of genes in parallel and are being used routinely to generate huge amounts of valuable data. Handling and analysis of such data are becoming major bottlenecks in the utilization of the technology. To enable the researcher to interpret the results postanalysis, we have developed a ***laboratory*** ***information*** ***management*** ***system*** for microarrays (LIMaS) with an n-tier Java front-end and relational database to record and manage large-scale expression data preanalysis. This system enables the laboratory to replace the paper trail with an efficient and fully customizable interface giving it the ability to adapt to any working practice, e.g., handling many resources used to form many products (chaining of resources). The ability to define sets of activities, resources, and workflows makes LIMaS MIAME-supportive.

L3 ANSWER 5 OF 74 MEDLINE on STN DUPLICATE 1
AN 2003248283 MEDLINE
DN PubMed ID: 12771210
TI SPINE 2: a system for collaborative structural proteomics within a federated database framework.
AU Goh Chern-Sing; Lan Ning; Echols Nathaniel; Douglas Shawn M; Milburn Duncan; Bertone Paul; Xiao Rong; Ma Li-Chung; Zheng Deyou; Wunderlich Zeba; Acton Tom; Montelione Gaetano T; Gerstein Mark
CS Molecular Biophysics and Biochemistry, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA.
SO Nucleic acids research, (2003 Jun 1) 31 (11) 2833-8.
Journal code: 0411011. ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200306
ED Entered STN: 20030529
Last Updated on STN: 20030701
Entered Medline: 20030630
AB We present version 2 of the SPINE system for structural proteomics. SPINE is available over the web at http://nesg.org. It serves as the central hub for the Northeast Structural Genomics Consortium, allowing collaborative structural proteomics to be carried out in a distributed fashion. The core of SPINE is a ***laboratory*** ***information*** ***management*** ***system*** (LIMS) for key bits of information

related to the progress of the consortium in cloning, expressing and purifying proteins and then solving their structures by NMR or X-ray crystallography. Originally, SPINE focused on tracking constructs, but, in its current form, it is able to track target sample tubes and store detailed sample histories. The core database comprises a set of standard relational tables and a data dictionary that form an initial ontology for proteomic properties and provide a framework for large-scale data mining. Moreover, SPINE sits at the center of a federation of interoperable information resources. These can be divided into (i) local resources closely coupled with SPINE that enable it to handle less standardized information (e.g. integrated mailing and publication lists), (ii) other information resources in the NESG consortium that are inter-linked with SPINE (e.g. crystallization LIMS local to particular laboratories) and (iii) international archival resources that SPINE links to and passes on information to (e.g. TargetDB at the PDB).

L3 ANSWER 6 OF 74 MEDLINE on STN DUPLICATE 2
AN 2003516612 MEDLINE
DN PubMed ID: 14594706
TI Development of an integrated ***laboratory*** ***information*** ***management*** ***system*** for the maize mapping project.
AU Sanchez-Villeda H; Schroeder S; Polacco M; McMullen M; Havermann S; Davis G; Vroh-Bi I; Cone K; Sharopova N; Yim Y; Schultz L; Duru N; Musket T; Houchins K; Fang Z; Gardiner J; Coe E
CS Department of Agronomy, Division of Biological Sciences and USDA-ARS, University of Missouri, Columbia, MO 65211, USA.
SO Bioinformatics (Oxford, England), (2003 Nov 1) 19 (16) 2022-30.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200404
ED Entered STN: 20031104
Last Updated on STN: 20040414
Entered Medline: 20040413
AB MOTIVATION: The development of an integrated genetic and physical map for the maize genome involves the generation of an enormous amount of data. Managing this data requires a system to aid in genotype scoring for different types of markers coming from both local and remote users. In addition, researchers need an efficient way to interact with genetic mapping software and with data files from automated DNA sequencing. They also need ways to manage primer data for mapping and sequencing and provide views of the integrated physical and genetic map and views of genetic map comparisons. RESULTS: The MMP-LIMS system has been used successfully in a high-throughput mapping environment. The genotypes from 957 SSR, 1023 RFLP, 189 SNP, and 177 InDel markers have been entered and verified via MMP-LIMS. The system is flexible, and can be easily modified to manage data for other species. The software is freely available. AVAILABILITY: To receive a copy of the iMap or cMap software, please fill out the form on our website. The other MMP-LIMS software is freely available at http://www.maizemap.org/bioinformatics.htm.

L3 ANSWER 7 OF 74 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2003:509676 BIOSIS
DN PREV200300510286
TI dbQSNP: A pipeline for SSCP based SNP-finding/quantification and publicizing allele frequency data of populations.
AU Tahira, T. [Reprint Author]; Baba, S. [Reprint Author]; Higasa, K. [Reprint Author]; Kukita, Y. [Reprint Author]; Suzuki, Y.; Sugano, S.; Hayashi, K. [Reprint Author]
CS Res Ctr Genet Info, Med Inst Bioreg, Kyushu Univ, Fukuoka, Japan
SO American Journal of Human Genetics, (November 2003) Vol. 73, No. 5, pp. 429. print.
Meeting Info.: 53rd Annual Meeting of the American Society of Human Genetics. Los Angeles, CA, USA. November 04-08, 2003. American Society of Human Genetics.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 29 Oct 2003
Last Updated on STN: 29 Oct 2003

L3 ANSWER 8 OF 74 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2003:417167 BIOSIS
DN PREV200300417167
TI Yeast structural genomics: High throughput production and crystallization of large sets of eukaryotic proteins.
AU van Tilbeurgh, H. [Reprint Author]
CS CNRS-UMR9920, Gif sur Yvette, France
SO European Biophysics Journal, (June 2003) Vol. 32, No. 3, pp. 173. print. Meeting Info.: 4th European Biophysics Congress. Alicante, Spain. July 05-09, 2003. European Biophysical Societies' Association (EBSA); Spanish Biophysics Society.
CODEN: EBJOE8. ISSN: 0175-7571.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 10 Sep 2003
Last Updated on STN: 10 Sep 2003

L3 ANSWER 9 OF 74 MEDLINE on STN DUPLICATE 3
AN 2003561433 MEDLINE
DN PubMed ID: 14649296
TI Secure web book to store structural genomics research data.
AU Manjasetty Babu A; Hoppner Klaus; Mueller Uwe; Heinemann Udo
CS Protein Structure Factory, c/o BESSY GmbH, Albert-Einstein Str.15, 12489, Berlin, Germany.
SO Journal of structural and functional genomics, (2003) 4 (2-3) 121-7.
Journal code: 101128185. ISSN: 1345-711X.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200407
ED Entered STN: 20031216
Last Updated on STN: 20040716
Entered Medline: 20040715
AB Recently established collaborative structural genomics programs aim at significantly accelerating the crystal structure analysis of proteins. These large-scale projects require efficient data management systems to ensure seamless collaboration between different groups of scientists working towards the same goal. Within the Berlin-based Protein Structure Factory, the synchrotron X-ray data collection and the subsequent crystal structure analysis tasks are located at BESSY, a third-generation synchrotron source. To organize file-based communication and data transfer at the BESSY site of the Protein Structure Factory, we have developed the web-based BCLIMS, the BESSY Crystallography ***Laboratory*** ***Information*** ***Management*** ***System*** . BCLIMS is a relational data management system which is powered by MySQL as the database engine and Apache HTTP as the web server. The database interface routines are written in Python programing language. The software is freely available to academic users. Here we describe the storage, retrieval and manipulation of laboratory information, mainly pertaining to the synchrotron X-ray diffraction experiments and the subsequent protein structure analysis, using BCLIMS.

L3 ANSWER 10 OF 74 MEDLINE on STN
AN 2003223379 MEDLINE
DN PubMed ID: 12744178
TI Design and realization of HL7 gateway.
AU Zhang Qing; Gao Shangkai
CS Institute of Biomedical Engineering, Tsinghua University, Beijing 100084.
SO Sheng wu yi xue gong cheng xue za zhi = Journal of biomedical engineering = Shengwu yixue gongchengxue zazhi, (2003 Mar) 20 (1) 111-5.
Journal code: 9426398. ISSN: 1001-5515.
CY China
DT Journal; Article; (JOURNAL ARTICLE)
LA Chinese
FS Priority Journals
EM 200308
ED Entered STN: 20030515
Last Updated on STN: 20030827
Entered Medline: 20030826
AB With the development of the technology in medical informatics area, Health Level Seven (HL7) Standard for electronic data exchange in all healthcare environments has become a widely used standard. To bring it into practice

in China, we developed an HL7 gateway. The gateway is used to connect two different medical information systems, a Hospital Information System (HIS) and a ***Laboratory*** ***Information*** ***Management*** ***System*** (LIMS), via the HL7 message exchanging. The system verified the feasibility of HL7 standard and made a good example for further research and development.

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=> d his

     (FILE 'HOME' ENTERED AT 14:24:45 ON 29 SEP 2004)

     FILE 'MEDLINE, BIOSIS' ENTERED AT 14:28:14 ON 29 SEP 2004
L1             1 S HIGH THROUGHPUT SCREENING AND LABORATORY INFORMATION MANAGEME
L2            86 S LABORATORY INFORMATION MANAGEMENT SYSTEM
L3            74 DUPLICATE REMOVE L2 (12 DUPLICATES REMOVED)

=> s l3 and py<2000
L4            43 L3 AND PY<2000

=> d 1-10 bib ab

L4   ANSWER 1 OF 43     MEDLINE on STN
AN   1998401068     MEDLINE
DN   PubMed ID: 9730921
TI   The LabBase system for data management in large scale biology research
     laboratories.
AU   Goodman N; Rozen S; Stein L D; Smith A G
CS   The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609-1500, USA,
     Whitehead Institute for Biomedical Research, Cambridge, MA, USA..
     nat@jax.org
SO   Bioinformatics (Oxford, England),   ***(1998)***   14 (7) 562-74.
     Journal code: 9808944. ISSN: 1367-4803.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199811
ED   Entered STN: 19990106
     Last Updated on STN: 19990106
     Entered Medline: 19981103
AB   MOTIVATION: The development of   ***laboratory***     ***information***
       ***management***     ***systems***   (LIMSs) for large scale biology
     research projects can be a challenging problem. Many such projects
     generate complex datasets via complex procedures that undergo continuous
     refinement. A key software challenge is to simplify the
     database-development task so that databases can be built and modified
     quickly enough to keep pace with changing project-requirements. Results:
     LabBase extends the facilities offered by relational database systems to
     simplify the task of creating databases for large scale biology research
     projects. LabBase provides a structural object data model, similar to
     ACEDB, and adds to this the concepts of Materials, Steps, and States:
     Materials are objects representing the identifiable things that
     participate in a laboratory protocol; Steps are objects reporting the
     results of a laboratory or analytical procedure; and States are objects
     denoting places in a laboratory protocol. The system provides a data
     definition language for succinctly defining laboratory databases, and
     operations for conveniently storing and retrieving data in such databases.
     The system also provides support for workflow management. LabBase is
     implemented in Perl5 and provides a natural interface for laboratory
     application programs written in Perl. AVAILABILITY: The software is
     freely available. Contact the authors. CONTACT: nat@jax.org

L4   ANSWER 2 OF 43     MEDLINE on STN
AN   1998391299     MEDLINE
DN   PubMed ID: 9725483
TI   LIMS: from theory to practice.
AU   Cardot J M; Hulot T; Le Bricon C; Stockis A
CS   Laboratoires CIBA-GEIGY, Rueil Malmaison, France.
SO   European journal of drug metabolism and pharmacokinetics,   ***(1998***
  ***      Apr-Jun)***   23 (2) 207-12.
     Journal code: 7608491. ISSN: 0398-7639.
CY   Switzerland
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
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FS Priority Journals
EM 199811
ED Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981103
AB This paper gives a definition and some basic knowledge about ***Laboratory*** ***Information*** ***Management*** ***Systems*** (LIMS) as well as their impact on the organisation, the laboratory and the co-workers. The major advantages and disadvantages of LIMS are pointed out. Two practical experiences are described. The first is related to an in house development of a PC based system which has to integrate a Vax VMS system (Multichrom) and PC based analytical and analysis softwares. The second experience is dealing with the selection and implementation of a commercial package in a pharmacokinetic laboratory. In both cases the human and time aspects were important.

L4 ANSWER 3 OF 43 MEDLINE on STN
AN 1998220408 MEDLINE
DN PubMed ID: 9556435
TI Validation of computer systems: practical testing of a standard LIMS.
AU Friedli D; Kappeler W; Zimmermann S
CS Spirig AG, Froschacker, Egerkingen, Switerzerland. szimmerm@cilch.jnj.com.
SO Pharmaceutica acta Helvetiae, ***(1998 Feb)*** 72 (6) 343-8.
Journal code: 0401134. ISSN: 0031-6865.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199804
ED Entered STN: 19980430
Last Updated on STN: 19980430
Entered Medline: 19980423
AB In recent years the introduction of computer systems for data handling in the pharmaceutical industry has increased. A standard LIMS (***laboratory*** ***information*** ***management*** ***system***) is software commercially available from different suppliers not only to facilitate data handling in laboratories but also to cover GMP-requirements. Computer systems introduced in GMP-areas of pharmaceutical companies have to be validated. For a standard LIMS, the general validation of the program is performed by the supplier. Nevertheless, the user is always required to cover all phases of a validation. The objective of this paper is to discuss suitable test procedures for the most critical functions of a standard LIMS needed during the verification step of the validation process.

L4 ANSWER 4 OF 43 MEDLINE on STN
AN 95079723 MEDLINE
DN PubMed ID: 7988110
TI Safety assessment of data management in a clinical laboratory.
AU Fink R
CS Department of Clinical Biochemistry, West Middlesex University Hospital, Isleworth, UK.
SO Computer methods and programs in biomedicine, ***(1994 Jul)*** 44 (1) 37-43.
Journal code: 8506513. ISSN: 0169-2607.
CY Ireland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199501
ED Entered STN: 19950124
Last Updated on STN: 19950124
Entered Medline: 19950111
AB This paper briefly reviews work undertaken within the DTI-sponsored MORSE project. The Clinical Biochemistry Department of the West Middlesex University Hospital, one of the five project partners, provides clinical and laboratory services to a wide range of users. The ***Laboratory*** ***Information*** ***Management*** ***System*** used within the department has been developed using a range of commercially available hardware and software together with software that has been designed and developed within the laboratory. This paper reports on the first stages of safety analysis of the overall operations in the laboratory. This is a pre-cursor to the systematic re-development of the information system in the light of the findings of the safety analysis.

L4 ANSWER 5 OF 43 MEDLINE on STN
AN 94278940 MEDLINE
DN PubMed ID: 8009645
TI DIAG, a ***laboratory*** ***information*** ***management*** ***system*** developed for regional animal disease diagnostic laboratories in Indonesia.
AU Hanks J D; Bedard B G; Navis S; Akoso B T; Putt S N; James A D; Heriyanto A
CS PAN Livestock Services Ltd, Department of Agriculture, Reading, England.
SO Tropical animal health and production, ***(1994 Feb)*** 26 (1) 13-9.
Journal code: 1277355. ISSN: 0049-4747.
CY SCOTLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199407
ED Entered STN: 19940729
Last Updated on STN: 19980206
Entered Medline: 19940718
AB The DIAG ***Laboratory*** ***Information*** ***Management*** ***System*** is a micro-computerised program designed for the use of regional and national animal disease diagnostic laboratories in Indonesia. It facilitates the day to day management of diagnostic data by monitoring the progress and turn round times of samples sent to laboratory sections and by printing outputs detailing the tests undertaken and results obtained. Notifiable disease reports are generated routinely as part of a national disease surveillance programme. Detailed analyses of specific diagnoses allow investigations of diseases over location and time. The database is easily accessed to allow additional analyses. Data entry is facilitated through the use of entry screens which reduce associated errors. The system is flexible and can readily be adapted to meet the demands of different countries, veterinary services and types of laboratory.

L4 ANSWER 6 OF 43 MEDLINE on STN
AN 94169256 MEDLINE
DN PubMed ID: 8123749
TI An update on ***laboratory*** ***information*** ***management*** ***systems*** .
AU McDowall R D
CS Department of Chemistry, University of Surrey, Guildford, UK.
SO Journal of pharmaceutical and biomedical analysis, ***(1993 Nov-Dec)*** 11 (11-12) 1327-30.
Journal code: 8309336. ISSN: 0731-7085.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199404
ED Entered STN: 19940420
Last Updated on STN: 19940420
Entered Medline: 19940414
AB The realization that a laboratory is an effective information generator within an organization has begun to influence the functions required of a ***laboratory*** ***information*** ***management*** ***system*** (LIMS): different laboratories require different functions. The trends in general computing such as open systems, adoption of relational database technology, and the use of more efficient development languages, are also impacting on the development of LIMS. These trends, plus the development of standards for both LIMS and analytical data interchange, will allow the development of systems that are quicker to implement, easier to maintain and meet the business need better.

L4 ANSWER 7 OF 43 MEDLINE on STN
AN 91083293 MEDLINE
DN PubMed ID: 2260832
TI The computerisation of scientific services.
AU Ng T L; Goh S C; Chow S T
CS Computer Centre, Institute of Science and Forensic Medicine, National Blood Centre, Singapore.
SO Annals of the Academy of Medicine, Singapore, ***(1990 Sep)*** 19 (5) 731-5.
Journal code: 7503289. ISSN: 0304-4602.
CY Singapore

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199101
ED Entered STN: 19910322
Last Updated on STN: 19910322
Entered Medline: 19910131
AB A full computerised ***laboratory*** ***information*** ***management*** ***system*** has been developed in the Department of Scientific Services. The system manages the acquisition and flow of laboratory data. A novel automated reporting procedure has been developed to generate customised laboratory reports. Based on the workload values of laboratory tests, the system integrates the laboratory data with management information to provide rapid and reliable productivity measurement and cost and pricing computations.

L4 ANSWER 8 OF 43 MEDLINE on STN
AN 90041472 MEDLINE
DN PubMed ID: 3268708
TI A ***laboratory*** ***information*** ***management*** ***system*** using memory cards.
AU Nishibori M; Shiina S
SO Rinsho byori. Japanese journal of clinical pathology, ***(1988 May)*** Spec No 77 91-101.
Journal code: 2984781R. ISSN: 0047-1860.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA Japanese
FS Priority Journals
EM 198912
ED Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19891205

L4 ANSWER 9 OF 43 MEDLINE on STN
AN 89359742 MEDLINE
DN PubMed ID: 2671006
TI Robotics in biomedical chromatography and electrophoresis.
AU Fouda H G
CS Drug Metabolism Department, Central Research, Pfizer Inc., Groton, CT 06340.
SO Journal of chromatography, ***(1989 Aug 11)*** 492 85-108. Ref: 90
Journal code: 0427043. ISSN: 0021-9673.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 198910
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19891010
AB The ideal laboratory robot can be viewed as "an indefatigable assistant capable of working continuously for 24 h a day with constant efficiency". The development of a system approaching that promise requires considerable skill and time commitment, a thorough understanding of the capabilities and limitations of the robot and its specialized modules and an intimate knowledge of the functions to be automated. The robot need not emulate every manual step. Effective substitutes for difficult steps must be devised. The future of laboratory robots depends not only on technological advances in other fields, but also on the skill and creativity of chromatographers and other scientists. The robot has been applied to automate numerous biomedical chromatography and electrophoresis methods. The quality of its data can approach, and in some cases exceed, that of manual methods. Maintaining high data quality during continuous operation requires frequent maintenance and validation. Well designed robotic systems can yield substantial increase in the laboratory productivity without a corresponding increase in manpower. They can free skilled personnel from mundane tasks and can enhance the safety of the laboratory environment. The integration of robotics, chromatography systems and ***laboratory*** ***information*** ***management*** ***systems*** permits full automation and affords opportunities for unattended method development and for future incorporation of artificial intelligence techniques and the evolution of expert systems. Finally,

humanoid attributes aside, robotic utilization in the laboratory should not be an end in itself. The robot is a useful tool that should be utilized only when it is prudent and cost-effective to do so.

L4 ANSWER 10 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1999:456799 BIOSIS
DN PREV199900456799
TI Hexalab ***laboratory*** ***information*** ***management*** ***system*** .
AU Ristic, P. [Reprint author]; Paunovic, M.; Stevic, B.; Velimirovic, I.; Boberic-borojevic, D.
CS Laboratory, Institute of Pharmacy of Serbia, Belgrade, Yugoslavia
SO Clinical Chemistry and Laboratory Medicine, (June, 1999) Vol. 37, No. SPEC. SUPPL., pp. S249. print.
Meeting Info.: IFC-WorldLab, International Federation of Clinical and Laboratory Medicine (17th International and 13th European Congress of Clinical Chemistry and Laboratory Medicine, 1st International Congress of Clinical Molecular Biology, 31st National Congress of the Italian Society of Clinical Biochemistry and Clinical Molecular Biology). Florence, Italy. June 6-11, 1999. International Federation of Clinical and Laboratory Medicine; Italian Society of Clinical Biochemistry and Clinical Molecular Biology.
ISSN: 1434-6621.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 1 Nov 1999
Last Updated on STN: 1 Nov 1999

=> d 11-20 bib ab

L4 ANSWER 11 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1999:126489 BIOSIS
DN PREV199900126489
TI Marker-assisted breeding to improve animal performance.
AU Walton, M.; Holm, T.
CS PE AgGen Inc., Applied DNA Serv., Salt Lake City, UT, USA
SO Animal Genetics, (Dec., 1998) Vol. 29, No. SUPPL. 1, pp. 2. print.
Meeting Info.: 26th International Conference on Animal Genetics. Auckland, New Zealand. August 9-14, 1998.
CODEN: ANGEE3. ISSN: 0268-9146.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 17 Mar 1999
Last Updated on STN: 17 Mar 1999

L4 ANSWER 12 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1998:416481 BIOSIS
DN PREV199800416481
TI Increase in quality and efficiency of daily workflow by making use of a paperless microbiology ***laboratory*** ***information*** ***management*** ***system*** .
AU Vogel, M.; Goessens, W. H. F.; Verbrugh, H. A.
CS Erasmus Univ. Med. Center Rotterdam, Rotterdam, Netherlands
SO Abstracts of the General Meeting of the American Society for Microbiology, (1998) Vol. 98, pp. 209. print.
Meeting Info.: 98th General Meeting of the American Society for Microbiology. Atlanta, Georgia, USA. May 17-21, 1998. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 2 Oct 1998
Last Updated on STN: 2 Oct 1998

L4 ANSWER 13 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AN 1998:173816 BIOSIS
DN PREV199800173816
TI Determination of soil pH using a Cartesian coordinate laboratory robot and electronic switchbox.
AU Quigley, Michael N. [Reprint author]; Reid, W. Shaw
CS Cornell Nutrient Anal. Lab., Dep. Soil Crop Atmospheric Sci., Bradfield Hall, Cornell Univ., Ithaca, NY 14853, USA
SO Communications in Soil Science and Plant Analysis, (Jan., 1998) Vol. 29, No. 1-2, pp. 211-217. print.
CODEN: CSOSA2. ISSN: 0010-3624.
DT Article
LA English
ED Entered STN: 6 Apr 1998
Last Updated on STN: 6 Apr 1998
AB A commercially available Cartesian coordinate (gantry style) robot has been programmed to sequentially determine soil/water pH (pHw) using a desk-top computer, electronic switchbox, pH meter and a bank of five combination electrodes. All movements of the robot together with pHw data acquisition are orchestrated by the computer. Once the pHw data has been acquired, it is stored in an array for subsequent transfer to a ***Laboratory*** ***Information*** ***Management*** ***System*** .

L4 ANSWER 14 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1997:420841 BIOSIS
DN PREV199799720044
TI LIMS for the biological laboratory.
AU Hayden, T.; Nelson, P. E.
SO FASEB Journal, (1997) Vol. 11, No. 9, pp. A1127.
Meeting Info.: 17th International Congress of Biochemistry and Molecular Biology in conjunction with the Annual Meeting of the American Society for Biochemistry and Molecular Biology. San Francisco, California, USA. August 24-29, 1997.
CODEN: FAJOEC. ISSN: 0892-6638.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 8 Oct 1997
Last Updated on STN: 8 Oct 1997

L4 ANSWER 15 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:455501 BIOSIS
DN PREV199699177857
TI A practical system for digital EEG laboratory information management.
AU Litt, B.; Ryan, D.; Hertz, S.; Beanland, C.; Hepner, D.; Van Sant, L.; Jones, P.; Lincoln, K.; McGuire, P.; Artemova, E.; Azizi, P.; Wityk, R.
CS Sinai Hosp. of Baltimore, Baltimore, MD, USA
SO Electroencephalography and Clinical Neurophysiology, (1996) Vol. 99, No. 2, pp. 11P.
Meeting Info.: 50th Annual Meeting of the Eastern Association of Electroecephalographers. St. Sauveur, Quebec, Canada. February 23, 1996.
CODEN: ECNEAZ. ISSN: 0013-4694.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 7 Oct 1996
Last Updated on STN: 7 Oct 1996

L4 ANSWER 16 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:213295 BIOSIS
DN PREV199698769424
TI Soilims: A low-budget, user-friendly ***laboratory*** ***information*** ***management*** ***system*** for small to medium-sized soil, plant, and water laboratories.
AU Brunt, J.; Van Reeuwijk, L. P.
CS International Soil Reference Information Cent., P.O. Box 353, 6700 AJ Wageningen, Netherlands
SO Communications in Soil Science and Plant Analysis, (1996) Vol. 27, No. 3-4, pp. 201-202.
Meeting Info.: International Symposium on Soil Testing and Plant Analysis: Quality of Soil and Plant Analysis in View of Sustainable Agriculture and the Environment, Part I. Wageningen, Netherlands. August 5-10, 1995.

CODEN: CSOSA2. ISSN: 0010-3624.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 2 May 1996
Last Updated on STN: 2 May 1996

L4 ANSWER 17 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:192773 BIOSIS
DN PREV199698748902
TI High throughput screening for new drug discovery.
AU Lin, Bing Bing
CS Panlabs Taiwan Ltd., 158 Li-Teh Rd., Pei-Tou, Taipei 112, Taiwan
SO Journal of Food and Drug Analysis, (1995) Vol. 3, No. 4, pp. 233-241.
ISSN: 1021-9498.
DT Article
LA English
ED Entered STN: 2 May 1996
Last Updated on STN: 2 May 1996
AB The world pharmaceutical market, which was valued at 247.9 billion in 1994, is forecasted to grow to 342 billion by 1999. High throughput screening(HTS) is attracting attention as a novel methodology for new drug discovery. HTS is expected to expand the scale from one thousand to one hundred thousand times the current level by utilizing robots, ***laboratory*** ***information*** ***management*** ***systems*** (LIMS), various sources to screen natural products(plant extracts, secondary microbial metabolites), peptide combinatorial libraries and combinatorial organic synthesis(COS) for new therapeutics. Instrumentation, target selection, source material, sample preparation, primary and secondary assays, isolation, purification and structure elucidation are all important for HTS.

L4 ANSWER 18 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:3997 BIOSIS
DN PREV199698576132
TI Implementation of a pharmacokinetic LIMS.
AU Lepsy, Christopher S.; Ryerson, Bruce A.; Gerts, Terry B.; Thompson, Paul R.; Nelson, Cindy
CS Pharmacokinetics and Drug Metabol. Dep., Parke-Davis Pharm. Res., Div. Warner Lambert Co., Ann Arbor, MI 48105, USA
SO Pharmaceutical Research (New York), (1995) Vol. 12, No. 9 SUPPL., pp. S364.
Meeting Info.: Annual Meeting of the American Association of Pharmaceutical Scientists. Miami Beach, Florida, USA. November 5-9, 1995.
CODEN: PHREEB. ISSN: 0724-8741.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 4 Jan 1996
Last Updated on STN: 4 Jan 1996

L4 ANSWER 19 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1995:133116 BIOSIS
DN PREV199598147416
TI Principal component analysis in the evaluation of environmental data.
AU Zitko, V.
CS Mar. Chem. Div., Phys. Chem. Sci. Branch, Dep. Fish. Oceans, Biol. Stn., St. Andrews, NB E0G 2X0, Canada
SO Marine Pollution Bulletin, (1994) Vol. 28, No. 12, pp. 718-722.
CODEN: MPNBAZ. ISSN: 0025-326X.
DT Article
LA English
ED Entered STN: 29 Mar 1995
Last Updated on STN: 29 Mar 1995
AB The objective of this article is to demonstrate by application to published data, the usefulness of Principal Component Analysis (PCA) in the examination of multivariate data. There is a number of monographs on the subject, as well as tutorials. The incorporation of PCA into ***Laboratory*** ***Information*** ***Management*** ***Systems*** (LIMS) at the data-to-information conversion stage, has been suggested. In spite of extensive literature, the use of PCA in the

evaluation of environmental data increases slowly. This article attempts to bridge the gap between the theory and the applications of PCA. It uses data published recently in this journal, to show how PCA can assist in their evaluation.

L4 ANSWER 20 OF 43 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1995:130894 BIOSIS
DN PREV199598145194
TI A LIMS for drug metabolism (BLIMS): The vendor perspective.
AU Broad, S. A.
CS Instem Computer Systems, Stone, Staffordshire ST15 0LT, UK
SO Chemometrics and Intelligent Laboratory Systems, (1994) Vol. 26, No. 3, pp. 165-169.
CODEN: CILSEN. ISSN: 0169-7439.
DT Article
Software Review
LA English
ED Entered STN: 29 Mar 1995
Last Updated on STN: 29 Mar 1995

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	44.41	45.67

STN INTERNATIONAL LOGOFF AT 14:42:12 ON 29 SEP 2004